

09/830,338
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Neurobiology: NAIP

NAIP (for neuronal apoptosis inhibitory protein) is a protein that inhibits apoptosis of neurons and its gene is often mutated in severe cases of spinal muscular atrophy, a disease characterized by motor neuron degeneration. NAIP is expressed in mouse macrophages, in anterior horn and motor cortex neurons of normal brains, in human fetal neurons and in adult choroid plexus cells. NAIP expression is increased after phagocytic events and during infection with *L. pneumophila*. There are at least three NAIP gene copies that encode full-length mRNA, NAIP1, 2, and 3.

Closest Matches:

Click on the **Product Name** to find out more information or to shop for a product.

Product	Cat.#	Isotype	Epitope	Applications	Species
NAIP2 (A-17)	sc-11068	goat IgG	internal (m)	WB, IHC	m, r
NAIP2 (T-17)	sc-11069	goat IgG	internal (m)	WB, IHC	m, r
NAIP1 (S-20)	sc-11067	goat IgG	N-terminus (m)	WB, IHC	m, r, h
NAIP1 (E-20)	sc-11066	goat IgG	N-terminus (m)	WB, IHC	m, r
NAIP (P-19)	sc-11064	goat IgG	C-terminus (h)	WB, IHC	m, r, h
NAIP (L-18)	sc-11062	goat IgG	N-terminus (m)	WB, IHC	m, r
NAIP (P-16)	sc-11059	goat IgG	N-terminus (h)	WB, IHC	m, r, h
NAIP (G-20)	sc-11060	goat IgG	C-terminus (h)	WB, IHC	h

Additional NAIP and related products:

Product	Cat.#	Isotype	Epitope	Applications	Species
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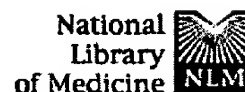


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- To combine searches use # before search number, e.g., #2 AND #6.
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Search	Most Recent Queries	Time	Result
	#8 Related Articles for PubMed (Select 9302277)	16:44:44	<u>198</u>
	#6 Related Articles for PubMed (Select 12547647)	16:39:35	<u>424</u>
	#4 Search #3 AND antibody	16:36:06	<u>1</u>
	#3 Related Articles for PubMed (Select 7813013)	16:35:34	<u>142</u>

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Dec 11 2003 12:53:39

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 09:11:50 (Search time 24 Seconds
2473.422 Million cell updates/sec
(without alignment))

Title: US-09-830-338-1

Perfect score: 1403
Sequence: 1 MATQKASDERISQFDHNL.....SKYTLTLQKWLPPSPITQK 1403

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size: 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database:

Issued Patents AA:*
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6: /cgn2_6/prodata/1/aa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	946	67.4	1232	3 US-08-836-134-2	Sequence 2, Appli
2	946	67.4	1232	4 US-09-493-784-2	Sequence 2, Appli
3	939	66.9	1151	3 US-08-836-134-23	Sequence 23, Appli
4	939	66.9	1151	4 US-09-493-784-23	Sequence 23, Appli
5	75	5.3	75	4 US-08-657-759-22	Sequence 24, Appli
6	56	4.0	56	4 US-08-657-759-24	Sequence 24, Appli
7	54	3.8	54	4 US-08-657-759-21	Sequence 21, Appli
8	50	3.6	50	3 US-08-975-080-26	Sequence 26, Appli
9	47	3.3	47	3 US-08-975-080-13	Sequence 13, Appli
10	20	1.4	20	4 US-08-657-759-20	Sequence 20, Appli
11	18	1.3	18	4 US-08-657-759-23	Sequence 23, Appli
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14	8	0.6	68	2 US-08-511-485-16	Sequence 16, Appli
15	8	0.6	68	4 US-09-201-936-16	Sequence 16, Appli
16	8	0.6	183	4 US-09-252-991A-24674	Sequence 24674, A
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18	8	0.6	428	4 US-09-461-240-18	Sequence 18, Appli
19	8	0.6	428	4 US-08-968-927-18	Sequence 18, Appli
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100	8	0.5	382	4 US-09-328-352-7438	Sequence 7438, Ap

ALIGNMENTS

RESULT 1

US-08-836-134-2

Sequence 2, Application US/08836134A

Patent No. 6020127

GENERAL INFORMATION:

APPLICANT: Mackenzie, Alex E.

APPLICANT: Korneluk, Robert G.

APPLICANT: Mahadevan, Mani S.

APPLICANT: McLean, Michael

APPLICANT: Roy, Natalie

APPLICANT: Ikeda, John-e

TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and

Patent No. 6020127

TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy

FILE REFERENCE: 3477-112, 033477/139914

CURRENT APPLICATION NUMBER: US/08/836,134A

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 1232

TYPE: PRT

ORGANISM: Homo sapiens

US-08-836-134-2

Query Match

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1146; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Score 946; DB 3; Length 1232;

67.4%;

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APPYNTVCLIKLPSHNMTRLRKPMYFGKNSLOKIOKTLPLVAAICAMHFOYEDPS 660

601

APPYNTVCLIKLPSHNMTRLRKPMYFGKNSLOKIOKTLPLVAAICAMHFOYEDPS 660

601

APPYNTVCLIKLPSHNMTRLRKPMYFGKNSLOKIOKTLPLVAAICAMHFOYEDPS 660

601

APPYNTVCLIKLPSHNMTRLRKPMYFGKNSLOKIOKTLPLVAAICAMHFOYEDPS 660

601

APPYNTVCLIKLPSHNMTRLRKPMYFGKNSLOKIOKTLPLVAAICAMHFOYEDPS 660

601

APPYNTVCLIKLPSHNMTRLRKPMYFGKNSLOKIOKTLPLVAAICAMHFOYEDPS 660

601

APPYNTVCLIKLPSHNMTRLRKPMYFGKNSLOKIOKTLPLVAAICAMHFOYEDPS 660

601

APPYNTVCLIKLPSHNMTRLRKPMYFGKNSLOKIOKTLPLVAAICAMHFOYEDPS 660

601

APPYNTVCLIKLPSHNMTRLRKPMYFGKNSLOKIOKTLPLVAAICAMHFOYEDPS 660

601

APPYNTVCLIKLPSHNMTRLRKPMYFGKNSLOKIOKTLPLVAAICAMHFOYEDPS 660

601

APPYNTVCLIKLPSHNMTRLRKPMYFGKNSLOKIOKTLPLVAAICAMHFOYEDPS 660

601

APPYNTVCLIKLPSHNMTRLRKPMYFGKNSLOKIOKTLPLVAAICAMHFOYEDPS 660

601

APPYNTVCLIKLPSHNMTRLRKPMYFGKNSLOKIOKTLPLVAAICAMHFOYEDPS 660

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

Q

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QY 1 MATOQKASDERISQFDHNLPELSALLGLDAVOLAKELEEBEOKERAMQKGYNSOMRSE 60
DB 1 MATOQKASDERISQFDHNLPELSALLGLDAVOLAKELEEBEOKERAMQKGYNSOMRSE 60
QY 61 AKRLKFTVYTPYSSWIPQEMAAAGFYTGVSGLIOCCSCSILIFGAGLTRPLIEDHKRF 120
DB 61 AKRLKFTVYTPYSSWIPQEMAAAGFYTGVSGLIOCCSCSILIFGAGLTRPLIEDHKRF 120
QY 121 HPDGGFLNLDVGNIAKYDIRVKNLSRLRGKMGVQEEBARLASFRNMPFYVGISPCV 180
DB 121 HPDGGFLNLDVGNIAKYDIRVKNLSRLRGKMGVQEEBARLASFRNMPFYVGISPCV 180
QY 181 LSEAGFYVTGKQDITVOCFSCGCGCLGWMEBGDDPMKEHAKMFKCEFLSKSSSEITQYI 240
DB 181 LSEAGFYVTGKQDITVOCFSCGCGCLGWMEBGDDPMKEHAKMFKCEFLSKSSSEITQYI 240
QY 241 OSYKGFVDITGEHFVNSWVORELPMASAYCNDISIFAYBELRLDSFKDMPRESAVGVALA 300
DB 241 OSYKGFVDITGEHFVNSWVORELPMASAYCNDISIFAYBELRLDSFKDMPRESAVGVALA 300
QY 301 KAGLFYTGIKDIOVOCFSCGCGCLEKMOEGDDPLDHTRCPCPNCPLONNKSSAEVTPDLOS 360
DB 301 KAGLFYTGIKDIOVOCFSCGCGCLEKMOEGDDPLDHTRCPCPNCPLONNKSSAEVTPDLOS 360
QY 361 RGEICELLETSESNLEDSIANGPIVEMAOGBAOMFOBAKXNLNQLAAATTSAPRMS 420
DB 361 RGEICELLETSESNLEDSIANGPIVEMAOGBAOMFOBAKXNLNQLAAATTSAPRMS 420
QY 421 LLDISSDLATDHLGCDLSTASKHISKPVOEPLVBEVGNINSVMCVGEAGSGKTVL 480
DB 421 LLDISSDLATDHLGCDLSTASKHISKPVOEPLVBEVGNINSVMCVGEAGSGKTVL 480
QY 481 KKIAPLWASGCCPLNRFOLVFTLSLSTRPDGLASIIICDULEKESVTEMCMRNIIQ 540
DB 481 KKIAPLWASGCCPLNRFOLVFTLSLSTRPDGLASIIICDULEKESVTEMCMRNIIQ 540
QY 541 QLNQVLEFLDDYKEICSIPOVIGKLIQKNHLSRTCLIAVETNRARDIRRYLETILEIK 600
DB 541 QLNQVLEFLDDYKEICSIPOVIGKLIQKNHLSRTCLIAVETNRARDIRRYLETILEIK 600
QY 601 AAPPNTVCIIRKLPNNMTLRKEMVYFGKNSLOKIOKTLFPAALCAHFOQPPRPS 660
DB 601 AAPPNTVCIIRKLPNNMTLRKEMVYFGKNSLOKIOKTLFPAALCAHFOQPPRPS 660
QY 661 FDDVAVFVSMEERLSLRNKAFAELIKATVSSCGELALKGFSCCEPFNDDILAEGVDED 720
DB 661 FDDVAVFVSMEERLSLRNKAFAELIKATVSSCGELALKGFSCCEPFNDDILAEGVDED 720
QY 721 EBLTNCMLSKFTQAORLRRPRRRLSPARQEFIAEMRLIBLDSROEHODLSYHLKOINS 780
DB 721 EBLTNCMLSKFTQAORLRRPRRRLSPARQEFIAEMRLIBLDSROEHODLSYHLKOINS 780
QY 781 PNMVTASANNFLANTVSSLPSTKAGPKIVSHLLHVDNKSLENISENDYTLKHQOEISIQ 840
DB 781 PNMVTASANNFLANTVSSLPSTKAGPKIVSHLLHVDNKSLENISENDYTLKHQOEISIQ 840
QY 841 MOLNGLMOICQAFPSWVSEHLLVTLAKTAYOSNTVAACSPVLOFLOGRSLTIGANTL 900
DB 841 MOLNGLMOICQAFPSWVSEHLLVTLAKTAYOSNTVAACSPVLOFLOGRSLTIGANTL 900
QY 901 QYFDPHPSLSILRSIHPIRGNKTSBRAHFSVLETCFDSQVPTIIDOVASAFEPNEM 960
DB 901 QYFDPHPSLSILRSIHPIRGNKTSBRAHFSVLETCFDSQVPTIIDOVASAFEPNEM 960
QY 961 BENLAEKEDNVKSWDMORBRASPDLSGWYKLSPKQYKPCLEVDVNDIDVYGOMLITL 1020
DB 961 BENLAEKEDNVKSWDMORBRASPDLSGWYKLSPKQYKPCLEVDVNDIDVYGOMLITL 1020
QY 1021 MTFVFSASORIEILHNSRGFTESIRPALLETSKASVTKCSISKLELSAABQELLLTLPSE 1080
DB 1021 MTFVFSASORIEILHNSRGFTESIRPALLETSKASVTKCSISKLELSAABQELLLTLPSE 1080
QY 1081 SLEVSGTIGSQOQIFPNLDKFLCKELSVLEGNINVSIVIPPEFPNFMHMKLLIQISA 1140

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DB 1081 SLEVSGTIGSQOQIFPNLDKFLCKELSVLEGNINVSIVIPPEFPNFMHMKLLIQISA 1140
QY 1141 EYDPSKLV 1148
DB 1141 EYDPSKLV 1148

RESULT 3
US-08-836-134-23
; Sequence 23, Application US/08836134A
; Patent No. 6020127
; GENERAL INFORMATION:
; APPLICANT: Mackenzie, Alex E.
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mahadevan, Mani S.
; APPLICANT: McLean, Michael
; APPLICANT: Roy, Natalie
; APPLICANT: Ikeda, John
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
; Patent No. 6020127
; TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
; FILE REFERENCE: 3477-112, 033477/139914
; CURRENT APPLICATION NUMBER: US/08/836,134A
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-836-134-23

Query Match 56.94; Score 939; DB 3; Length 1151;
Best Local Similarity 99.81; Pred. No. 0;
Matches 1139; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATOQKASDERISQFDHNLPELSALLGLDAVOLAKELEEBEOKERAMQKGYNSOMRSE 60
DB 1 MATOQKASDERISQFDHNLPELSALLGLDAVOLAKELEEBEOKERAMQKGYNSOMRSE 60
QY 61 AKRLKFTVYTPYSSWIPQEMAAAGFYTGVSGLIOCCSCSILIFGAGLTRPLIEDHKRF 120
DB 61 AKRLKFTVYTPYSSWIPQEMAAAGFYTGVSGLIOCCSCSILIFGAGLTRPLIEDHKRF 120
QY 121 HPDGGFLNLDVGNIAKYDIRVKNLSRLRGKMGVQEEBARLASFRNMPFYVGISPCV 180
DB 121 HPDGGFLNLDVGNIAKYDIRVKNLSRLRGKMGVQEEBARLASFRNMPFYVGISPCV 180
QY 181 LSEAGFYVTGKQDITVOCFSCGCGCLGWMEBGDDPMKEHAKMFKCEFLSKSSSEITQYI 240
DB 181 LSEAGFYVTGKQDITVOCFSCGCGCLGWMEBGDDPMKEHAKMFKCEFLSKSSSEITQYI 240
QY 241 OSYKGFVDITGEHFVNSWVORELPMASAYCNDISIFAYBELRLDSFKDMPRESAVGVALA 300
DB 241 OSYKGFVDITGEHFVNSWVORELPMASAYCNDISIFAYBELRLDSFKDMPRESAVGVALA 300
QY 301 KAGLFYTGIKDIOVOCFSCGCGCLEKMOEGDDPLDHTRCPCPNCPLONNKSSAEVTPDLOS 360
DB 301 KAGLFYTGIKDIOVOCFSCGCGCLEKMOEGDDPLDHTRCPCPNCPLONNKSSAEVTPDLOS 360
QY 361 RGEICELLETSESNLEDSIANGPIVEMAOGBAOMFOBAKXNLNQLAAATTSAPRMS 420
DB 361 RGEICELLETSESNLEDSIANGPIVEMAOGBAOMFOBAKXNLNQLAAATTSAPRMS 420
QY 421 LLDISSDLATDHLGCDLSTASKHISKPVOEPLVBEVGNINSVMCVGEAGSGKTVL 480
DB 421 LLDISSDLATDHLGCDLSTASKHISKPVOEPLVBEVGNINSVMCVGEAGSGKTVL 480
QY 481 KKIAPLWASGCCPLNRFOLVFTLSLSTRPDGLASIIICDULEKESVTEMCMRNIIQ 540
DB 481 KKIAPLWASGCCPLNRFOLVFTLSLSTRPDGLASIIICDULEKESVTEMCMRNIIQ 540
QY 540 KKIAPLWASGCCPLNRFOLVFTLSLSTRPDGLASIIICDULEKESVTEMCMRNIIQ 549

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QY 541 OLKNOVLFLDDYKEICSIPOVIGKLIQKNHLSRTCLLIARTNRARDIRRYLETILEIK 600
 DB 550 QIKNOVLFLDDYKEICSIPOVIGKLIQKNHLSRTCLLIARTNRARDIRRYLETILEIQ 609
 QY 601 APEPVNTVCILRLKLSHNMTRLRKFMVYFGKNOSLOKIOKTPLEFVAICAHFOYPPDS 660
 DB 610 APEPVNTVCILRLKLSHNMTRLRKFMVYFGKNOSLOKIOKTPLEFVAICAHFOYPPDS 669
 QY 661 FDDVAVFKSYMERLSLRNKATABILKATVSGCELAIKGFSCCFEFDNDLAEAGVED 720
 DB 670 FDDVAVFKSYMERLSLRNKATABILKATVSGCELAIKGFSCCFEFDNDLAEAGVED 729
 QY 721 EDLTMCLMSKFTAQRLRPFRFLSPAFQEFLLAEMLIELDSDROQHODGLYHLKOINS 780
 DB 730 EDLTMCLMSKFTAQRLRPFRFLSPAFQEFLLAEMLIELDSDROQHODGLYHLKOINS 789
 QY 781 PMMTVSAYNNFLNTVSSLPSTKAGPKVSHLHLVDNKSLENISENDYLGKQPEISLQ 840
 DB 790 PMMTVSAYNNFLNTVSSLPSTKAGPKVSHLHLVDNKSLENISENDYLGKQPEISLQ 849
 QY 841 MOLLRLGLMOICPOAYFSWSEHLVLALKTAYOSNTVAACSPVLQFLOGRTLTGALNL 900
 DB 850 MOLLRLGLMOICPOAYFSWSEHLVLALKTAYOSNTVAACSPVLQFLOGRTLTGALNL 909
 QY 901 QYFPHPSLSLRSIHPIRGNTSPRAHFSVLETCFDKSOVPTTIDODYASAFPMNEM 960
 DB 910 QYFPHPSLSLRSIHPIRGNTSPRAHFSVLETCFDKSOVPTTIDODYASAFPMNEM 969
 QY 961 ERNLAEKEDNVKSYMDMORRASPDLSTGYWKLSPKOYKIPCLEVDVNDIDVQODMLEIL 1020
 DB 970 ERNLAEKEDNVKSYMDMORRASPDLSTGYWKLSPKOYKIPCLEVDVNDIDVQODMLEIL 1029
 QY 1021 MTPVASORIEHLNHSRGFTESIRPLAELSKSVYKCSISKLELSAAQBELLTLPSE 1080
 DB 1030 MTPVASORIEHLNHSRGFTESIRPLAELSKSVYKCSISKLELSAAQBELLTLPSE 1089
 QY 1081 SLEVSGTIOQODOIFPNLDKFLCKELSVDLBGNINVFVPIPEEPFNHMEKLLIQISA 1140
 DB 1090 SLEVSGTIOQODOIFPNLDKFLCKELSVDLBGNINVFVPIPEEPFNHMEKLLIQISA 1149
 QY 1141 E 1141
 DB 1150 E 1150
 RESULT 4
 US-09-493-784-23
 ; Sequence 23, Application US/09493784
 ; Patent No. 6429011
 ; GENERAL INFORMATION:
 ; APPLICANT: Mackenzie, Alex E.
 ; APPLICANT: Korneljuk, Robert G.
 ; APPLICANT: Mahadevan, Mani S.
 ; APPLICANT: McLean, Michael
 ; APPLICANT: Roy, Natalie
 ; APPLICANT: Ikeda, John
 ; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
 ; Patent No. 6429011
 ; FILE REFERENCE: Mutations Causing of Spinal Muscular Atrophy
 ; CURRENT FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: US/09/493,784
 ; PRIOR FILING DATE: 1997-06-20
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 23
 ; LENGTH: 1151
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-493-784-23
 Query Match 66.9%; Score 939; DB 4; Length 1151;

Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1139; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MATOOKASDERISQFDNNILPELSALIGDAVOLAKLEEFEEQKRAMQGYNSQMRSE 60
 DB 10 MATOOKASDERISQFDNNILPELSALIGDAVOLAKLEEFEEQKRAMQGYNSQMRSE 69
 QY 61 AKRLKTPVYEPYBSWIPQEMAAAGFPYGVNSGICQFCCSLILFAGLITRLPIEDKRP 120
 DB 70 AKRLKTPVYEPYBSWIPQEMAAAGFPYGVNSGICQFCCSLILFAGLITRLPIEDKRP 129
 QY 121 HPDGGFLNDVGNIAKYDIRVKNLSRGRKMFVQREBARLASFRMPPYVGISPCV 180
 DB 130 HPDGGFLNDVGNIAKYDIRVKNLSRGRKMFVQREBARLASFRMPPYVGISPCV 189
 QY 181 LSEAGFVFTGKODTVQCFSCGGLGNMBEGDDPMKHAHAKFPKCSPLRSKKSSEITQYI 240
 DB 190 LSEAGFVFTGKODTVQCFSCGGLGNMBEGDDPMKHAHAKFPKCSPLRSKKSSEITQYI 249
 QY 241 QSYKGFVDITGEHFVNSWVQRELPNMAAYCNDSTIAYEELRLDSFKDMPRESAYGVALA 300
 DB 250 QSYKGFVDITGEHFVNSWVQRELPNMAAYCNDSTIAYEELRLDSFKDMPRESAYGVALA 309
 QY 301 KAGLPTTGIDIVQCFSCGGLCEKMOEGDDPLDHTRCFPNCPLONNKSSAEVTPDIQS 360
 DB 310 KAGLPTTGIDIVQCFSCGGLCEKMOEGDDPLDHTRCFPNCPLONNKSSAEVTPDIQS 369
 QY 361 RGECELLETTSESNEJDSIANGPIYPEMAQGEAOMPOBARNLNEOLRAATYSFRHMS 420
 DB 370 RGECELLETTSESNEJDSIANGPIYPEMAQGEAOMPOBARNLNEOLRAATYSFRHMS 429
 QY 421 LLDISDLDTHLIGCDLSTASGRHSKVPQEPVLVPEVGNLNSVMCEBAGSGKTALL 480
 DB 430 LLDISDLDTHLIGCDLSTASGRHSKVPQEPVLVPEVGNLNSVMCEBAGSGKTALL 489
 QY 481 KKIAPLWASGCCPLNRPOLVFLYLSSTRPEGLASITICQULEKESGVTBEMCRNIQ 540
 DB 490 KKIAPLWASGCCPLNRPOLVFLYLSSTRPEGLASITICQULEKESGVTBEMCRNIQ 549
 QY 541 OLKNOVLFLDDYKEICSIPOVIGKLIQKNHLSRTCLLIARTNRARDIRRYLETILEIK 600
 DB 550 OLKNOVLFLDDYKEICSIPOVIGKLIQKNHLSRTCLLIARTNRARDIRRYLETILEIQ 609
 QY 601 APEPVNTVCILRLKLSHNMTRLRKFMVYFGKNOSLOKIOKTPLEFVAICAHFOYPPDS 660
 DB 610 APEPVNTVCILRLKLSHNMTRLRKFMVYFGKNOSLOKIOKTPLEFVAICAHFOYPPDS 669
 QY 661 FDDVAVFKSYMERLSLRNKATABILKATVSGCELAIKGFSCCFEFDNDLAEAGVED 720
 DB 670 FDDVAVFKSYMERLSLRNKATABILKATVSGCELAIKGFSCCFEFDNDLAEAGVED 729
 QY 721 EDLTMCLMSKFTAQRLRPFRFLSPAFQEFLLAEMLIELDSDROQHODGLYHLKOINS 780
 DB 730 EDLTMCLMSKFTAQRLRPFRFLSPAFQEFLLAEMLIELDSDROQHODGLYHLKOINS 789
 QY 781 PMMTVSAYNNFLNTVSSLPSTKAGPKVSHLHLVDNKSLENISENDYLGKQPEISLQ 840
 DB 790 PMMTVSAYNNFLNTVSSLPSTKAGPKVSHLHLVDNKSLENISENDYLGKQPEISLQ 849
 QY 841 MOLLRLGLMOICPOAYFSWSEHLVLALKTAYOSNTVAACSPVLQFLOGRTLTGALNL 900
 DB 850 MOLLRLGLMOICPOAYFSWSEHLVLALKTAYOSNTVAACSPVLQFLOGRTLTGALNL 909
 QY 901 QYFPHPSLSLRSIHPIRGNTSPRAHFSVLETCFDKSOVPTTIDODYASAFPMNEM 960
 DB 910 QYFPHPSLSLRSIHPIRGNTSPRAHFSVLETCFDKSOVPTTIDODYASAFPMNEM 969
 QY 961 ERNLAEKEDNVKSYMDMORRASPDLSTGYWKLSPKOYKIPCLEVDVNDIDVQODMLEIL 1020
 DB 970 ERNLAEKEDNVKSYMDMORRASPDLSTGYWKLSPKOYKIPCLEVDVNDIDVQODMLEIL 1029
 QY 1021 MTPVASORIEHLNHSRGFTESIRPLAELSKSVYKCSISKLELSAAQBELLTLPSE 1080

DB 1030 MTVPASQRIEIHNSRGPIESIRPALBLSKASVTKSISKLELSAAEQLLLTLPSE 1089
QY 1081 SLEVSCTIGSQDQIPPLDLKFLCKELSYDLGNINVSVPPEEPNFHMEKLLIOISA 1140
DB 1090 SLEVSCTIGSQDQIPPLDLKFLCKELSYDLGNINVSVPPEEPNFHMEKLLIOISA 1149
QY 1141 E 1141
DB 1150 E 1150

RESULT 5
US-08-657-759-22
; Sequence 22, Application US/08657759
; Patent No. 6511828
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,759
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 75 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-657-759-22

Query Match 5.3%; Score 75; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.6e-64;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 QEEERARLASPPNWFYQGISPCVLSSEAGVFPFGKQDTYQCGSCGCGCIGNNEBGDDPWKE 216
DB 1 QEEERARLASPPNWFYQGISPCVLSSEAGVFPFGKQDTYQCGSCGCGCIGNNEBGDDPWKE 60
QY 217 HAKWFPKCEPLRSKX 231
DB 61 HAKWFPKCEPLRSKX 75

RESULT 6
US-08-657-759-24
; Sequence 24, Application US/08657759
; Patent No. 6511828
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Duckett, Colin S.
; TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS

; TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,759
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-657-759-24

Query Match 4.0%; Score 56; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.1e-46;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 VGVAAALAKAGLFTYGTGKIDIVQCFSCGCGCLEKMQEGDDPLDHTFCPPNCFPLQMK 349
DB 1 VGVAAALAKAGLFTYGTGKIDIVQCFSCGCGCLEKMQEGDDPLDHTFCPPNCFPLQMK 56

RESULT 7
US-08-657-759-21
; Sequence 21, Application US/08657759
; Patent No. 6511828
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Duckett, Colin S.
; TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,759
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:220
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-657-759-21

Query Match 3.8%; Score 54; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.4e-44;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 PGMMAAGFYTGVSGLQCCSLIFGAGLTRLPIDHKKRPHPCGFLNKD 131
DB 1 PGMMAAGFYTGVSGLQCCSLIFGAGLTRLPIDHKKRPHPCGFLNKD 54

RESULT 8
US-08-975-080-26
Sequence 26, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-080-26

Query Match 3.6%; Score 50; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e-40;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 YTGIDIVQCFSCGCKEKNOQBDPLDHTRCFPCPLQMKSSAEVT 355
DB 1 YTGIDIVQCFSCGCKEKNOQBDPLDHTRCFPCPLQMKSSAEVT 50

RESULT 9
US-08-975-080-13

Sequence 13, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-080-13

Query Match 3.3%; Score 47; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.7e-37;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 BEARLASFRWPFYVGGISPCVLSBAGFVFTGKOPTVQCFSCGCLG 205
DB 1 BEARLASFRWPFYVGGISPCVLSBAGFVFTGKOPTVQCFSCGCLG 47

RESULT 10
US-08-657-759-20
Sequence 20, Application US/08657759
Patent No. 6511828
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
APPLICANT: Duckett, Colin S.
TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
OF APOPTOSIS PROTEINS (IAPs)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,759
FILING DATE: 31-MAY-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-657-759-20

Query Match 1.4%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 RSEAKRLKTFYTPYSSWI 77
DB 1 RSEAKRLKTFYTPYSSWI 20

RESULT 11
US-08-657-759-23
Sequence 23, Application US/08657759
Patent No. 6511828
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
APPLICANT: Duckett, Colin S.
TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,759
FILING DATE: 31-MAY-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-657-759-23

Query Match 1.3%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 AYEBRLUDSFQWPRSA 293

DB 1 AYEBRLUDSFQWPRSA 18

RESULT 12
US-09-252-991A-28407
Sequence 28407, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28407
LENGTH: 870
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28407

Query Match 0.6%; Score 9; DB 4; Length 870;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 472 AGSGKTVLL 480
DB 55 AGSGKTVLL 63

RESULT 13
US-09-205-258-580
Sequence 580, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06

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/ EARLIER APPLICATION NUMBER: 60/048,899
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,893
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,900
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,901
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,892
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,915
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,019
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,970
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,972
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,916
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,373
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,875
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,374
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,917
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,949
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,974
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,883
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,897
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,898
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,962
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,963
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,877
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,878
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/070,923
/ EARLIER FILING DATE: 1997-12-18
/ EARLIER APPLICATION NUMBER: 60/092,921
/ EARLIER FILING DATE: 1998-07-15
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ NUMBER OF SEQ ID NOS: 1227
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 580
/ LENGTH: 64
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-205-258-580

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Query Match      0.6% Score 8; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 39 EEEEOKKER 46
    |||||
Db 29 EEEEOKKER 36

```

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RESULT 14
US-08-511-485-16
/ Sequence 16, Application US/08511485
/ Patent No. 5919912

```

```

/ GENERAL INFORMATION:
/ APPLICANT: Korneluk, Robert G.
/ APPLICANT: Mackenzie, Alexander E.
/ APPLICANT: Baird, Stephen
/ TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
/ NUMBER OF SEQUENCES: 38
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: Fish & Richardson P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/511,485
/ FILING DATE: 04-AUG-1995
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617/542-5070
/ TELEFAX: 617/542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 68 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: both
/ MOLECULE TYPE: protein
US-08-511-485-16

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```

Query Match      0.6% Score 8; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 193 DTVQCFCSC 200
    |||||
Db 34 DTVQCFCSC 41

```

```

RESULT 15
US-09-201-936-16
/ Sequence 16, Application US/09201936
/ Patent No. 6541457
/ GENERAL INFORMATION:
/ APPLICANT: Korneluk, Robert G.
/ APPLICANT: Mackenzie, Alexander E.
/ APPLICANT: Baird, Stephen
/ APPLICANT: Iason, Peter
/ TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
/ FILE REFERENCE: 07891/003003
/ CURRENT APPLICATION NUMBER: US/09/201,936
/ CURRENT FILING DATE: 1998-12-01
/ EARLIER APPLICATION NUMBER: 09/011,356
/ EARLIER FILING DATE: 1998-02-04
/ EARLIER APPLICATION NUMBER: PCT/IB96/01022
/ EARLIER FILING DATE: 1996-08-05
/ EARLIER APPLICATION NUMBER: 08/576,956
/ EARLIER FILING DATE: 1995-12-22
/ EARLIER APPLICATION NUMBER: 08/511,485
/ EARLIER FILING DATE: 1995-08-04
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: FastSeq for Windows Version 3.0

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SEQ ID NO 16
LENGTH: 68
TYPE: PRT
ORGANISM: Mus musculus
US-09-201-936-16

Query Match 0.6%; Score 8; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 DTVOCFSC 200
Db 34 DTVOCFSC 41

RESULT 16
US-09-253-991A-24674
Sequence 24674, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A

PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074.788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094.190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24674
LENGTH: 183

TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24674

Query Match 0.6%; Score 8; DB 4; Length 183;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 504 LSLSTRP 511
Db 154 LSLSTRP 161

RESULT 17
US-08-301-162-18

Sequence 18, Application US/08301162
Patent No. 6022546

GENERAL INFORMATION:
APPLICANT: Knapp, Stefan
APPLICANT: Ziegelmair, Robert
TITLE OF INVENTION: Toxoplasma Gondii Antigens, The
TITLE OF INVENTION: Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/301.162
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/167.128

FILING DATE:
APPLICATION NUMBER: US 07/623.086
FILING DATE: 06-DEC-1990
APPLICATION NUMBER: DE P3940598.2
FILING DATE: 08-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleishner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 02481.1005-00000

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-301-162-18

Query Match 0.6%; Score 8; DB 3; Length 428;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FGAGLTRL 112
Db 395 FGAGLTRL 402

RESULT 18
US-09-461-240-18

Sequence 18, Application US/09461240
Patent No. 6326008

GENERAL INFORMATION:
APPLICANT: Knapp, Stefan
APPLICANT: Ziegelmair, Robert
TITLE OF INVENTION: Toxoplasma Gondii Antigens, The
TITLE OF INVENTION: Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/461.240
FILING DATE: 16-DEC-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/301.162
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/623.086

FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/623.086
FILING DATE: 06-DEC-1990
APPLICATION NUMBER: DE P3940598.2

FILING DATE: 08-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleishner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 02481.1005-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4400

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 428 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-461-240-18

Query Match

Best Local Similarity 100.0%; Score 8; DB 4; Length 428;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 105 FGAGLTRL 112

Db 395 FGAGLTRL 402

RESULT 19

US-09-968-927-18

Sequence 18, Application US/09968927

Patent No. 6419925

GENERAL INFORMATION:

APPLICANT: Knapp, Stefan

Ziegelmaier, Robert

Kupper, Hans

TITLE OF INVENTION: Toxoplasma Gondii Antigen, The

Preparation Thereof and the Use Thereof

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSER: Finnegan, Henderson, Farabow, Garrett &

Dunne

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/968,927

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/301,162

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/157,128

FILING DATE: <Unknown>

APPLICATION NUMBER: US 07/623,086

FILING DATE: 06-DEC-1990

APPLICATION NUMBER: DE P3940598.2

FILING DATE: 08-DEC-1989

ATTORNEY/AGENT INFORMATION:

NAME: Fleisher, Raz E.

REGISTRATION NUMBER: 34,331

REFERENCE/DOCKET NUMBER: 02481.1005-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4400

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 428 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-968-927-18

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4400

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 428 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-461-240-18

Query Match

Best Local Similarity 100.0%; Score 8; DB 4; Length 428;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 105 FGAGLTRL 112

Db 395 FGAGLTRL 402

RESULT 20

US-09-198-452A-170

Sequence 170, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffiths, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 170

LENGTH: 441

TYPE: PR

ORGANISM: Chlamydia pneumoniae

US-09-198-452A-170

Query Match

Best Local Similarity 100.0%; Score 8; DB 4; Length 441;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 102 LILFGAGL 109

Db 135 LILFGAGL 142

RESULT 21

US-08-511-485-10

Sequence 10, Application US/08511485

Patent No. 5919912

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: Mackenzie, Alexander E.

APPLICANT: Baird, Stephen

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSER: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/511,485

FILING DATE: 04-AUG-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 07540/002001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-10

Query Match 0.64; Score 8; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSC 200
Db 59 DTVOCFSC 66

RESULT 22
US-09-212-971-10
Sequence 10, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
US-09-212-971-10

Query Match 0.64; Score 8; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSC 200
Db 59 DTVOCFSC 66

RESULT 23
US-08-800-929A-10
Sequence 10, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/08/800,929
CURRENT FILING DATE: 2000-07-14
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
US-09-617-053A-10

CORRESPONDENCE ADDRESS:
ADDRESSER: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-929A-10

Query Match 0.64; Score 8; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSC 200
Db 59 DTVOCFSC 66

RESULT 24
US-09-617-053A-10
Sequence 10, Application US/09617053A
Patent No. 6300492
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
US-09-617-053A-10

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Query Match      0.64; Score 8; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 54;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      193 DTVOCFSC 200
Db      59 DTVOCFSC 66

RESULT 25
US-09-201-936-10
; Sequence 10, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN TAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/1996/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-10

Query Match      0.64; Score 8; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 54;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      193 DTVOCFSC 200
Db      59 DTVOCFSC 66

RESULT 26
US-09-205-258-573
; Sequence 573, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007p1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 573
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
```

NAME/KEY: SITE
LOCATION: (409)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-573

Query Match 0.6%; Score 8; DB 4; Length 567;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEOKER 46
DB 483 EEEOKER 490

RESULT 27
US-09-303-064-55
Sequence 55, Application US/09303064
Patent No. 6221619
GENERAL INFORMATION:
APPLICANT: MAINE, Gregory T.
APPLICANT: HUNT, Jeffery C.
APPLICANT: BROJANAC, Susan
APPLICANT: JYH-TSING SHEU, Michael
APPLICANT: CHOVAN, Linda E.
APPLICANT: TYNER, Joan D.
APPLICANT: HOWARD, Lawrence V.
APPLICANT: PARMELEY, Stephen F.
APPLICANT: REMINGTON, Jack S.
APPLICANT: ARAUJO, Fausto
APPLICANT: SUZUKI, Yasuhiko
APPLICANT: LI, Shuli
TITLE OF INVENTION: ANTIGEN COCKTAILS, P35 AND USES THEREOF
FILE REFERENCE: 6361.US.P1
CURRENT APPLICATION NUMBER: US/09/303,064
CURRENT FILING DATE: 1999-04-30
EARLIER APPLICATION NUMBER: 09/086,503
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 55
LENGTH: 667
TYPE: PRT
ORGANISM: Toxoplasma gondii
US-09-303-064-55

Query Match 0.6%; Score 8; DB 3; Length 667;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FGAGLTRL 112
DB 542 FGAGLTRL 549

RESULT 28
US-09-086-503-55
Sequence 55, Application US/09086503A
Patent No. 6329157
GENERAL INFORMATION:
APPLICANT: MAINE, Gregory T.
APPLICANT: HUNT, Jeffery C.
APPLICANT: BROJANAC, Susan
APPLICANT: JYH-TSING SHEU, Michael
APPLICANT: CHOVAN, Linda E.
APPLICANT: TYNER, Joan D.
APPLICANT: HOWARD, Lawrence V.
TITLE OF INVENTION: ANTIGEN COCKTAILS AND USES THEREOF
FILE REFERENCE: 6361.US.01
CURRENT APPLICATION NUMBER: US/09/086,503A
CURRENT FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 55

LENGTH: 667
TYPE: PRT
ORGANISM: Toxoplasma gondii
US-09-086-503-55

Query Match 0.6%; Score 8; DB 4; Length 667;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FGAGLTRL 112
DB 542 FGAGLTRL 549

RESULT 29
US-08-434-730-14
Sequence 14, Application US/08434730
Patent No. 3637463
GENERAL INFORMATION:
APPLICANT: Dalton, Stephen
APPLICANT: Kochan, Jarema P
APPLICANT: Osborn, Mark A
TITLE OF INVENTION: METHOD TO DETECT PROTEIN-PROTEIN
INTERACTIONS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc
STREET: 340 Kingsland street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,730
FILING DATE: 04-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Semionow, Raina
REGISTRATION NUMBER: 39022
REFERENCE/DOCKET NUMBER: 9069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)235-4391
TELEFAX: (201)235-2363
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 968 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-434-730-14

Query Match 0.6%; Score 8; DB 1; Length 968;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1075 TLPLSLSL 1082
DB 229 TLPLSLSL 236

RESULT 30
US-08-560-005-2
Sequence 2, Application US/08560005
Patent No. 6001354
GENERAL INFORMATION:
APPLICANT: Pot David A.
APPLICANT: Williams, Lewis T.

APPLICANT: Jefferson, Anne Bennett
TITLE OF INVENTION: No. 6001354el Grb2 Associating Protein and Nucleic
NUMBER OF SEQUENCES: 10
ADDRESS: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,005
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-0624000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 976 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-560-005-2

Query Match
Best Local Similarity 0.64; Score 8; DB 3; Length 976;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1075 TLPSLESL 1082
DB 14 TLPSLESL 21

RESULT 31
US-09-195-868-14
Sequence 14, Application US/09195868
Patent No. 6090621
GENERAL INFORMATION:
APPLICANT: KAVANAUGH MD, MICHAEL
APPLICANT: POT PH.D., DAVID
APPLICANT: WILLIAMS M.D., LEWIS T.
TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 HORTON STREET
CITY: EMERYVILLE
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,868
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US/09/195,868

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PIRBSTONE, LEIGH H.
REGISTRATION NUMBER: 36,831
REFERENCE/DOCKET NUMBER: 1182,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-923-2707
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 976 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-195-868-14

Query Match
Best Local Similarity 0.64; Score 8; DB 3; Length 976;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1075 TLPSLESL 1082
DB 14 TLPSLESL 21

RESULT 32
US-09-418-540-2
Sequence 2, Application US/09418540
Patent No. 6296848
GENERAL INFORMATION:
APPLICANT: Pot, David A.
APPLICANT: WILLIAMS, Lewis T.
APPLICANT: Jefferson, Anne Bennett
TITLE OF INVENTION: No. 6296848el Grb2 Associating Protein and Nucleic
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/418,540
FILING DATE: 14-OCT-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/560,005
FILING DATE: 17-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-0624000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 976 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-418-540-2

Query Match 0.64; Score 8; DB 3; Length 976;

Best Local Similarity 100.0%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1075 TLPSLESL 1082
DB 14 TLPSLESL 21

RESULT 33

US-09-969-528-2
Sequence 2, Application US/09969528
Patent No. 6472197
GENERAL INFORMATION:
APPLICANT: Pot, David A.
Williams, Lewis T.
Jefferson, Anne Bennett
Maierus, Philip W.
TITLE OF INVENTION: No. 6472197el Grd2 Associating Protein and Nucleic
Acids Encoding Therefor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESS: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,528
FILING DATE: 01-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/560,005
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-0624000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 976 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-969-528-2

Query Match 0.6%; Score 8; DB 4; Length 976;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1075 TLPSLESL 1082
DB 14 TLPSLESL 21

RESULT 34

US-08-664-962B-2
Sequence 2, Application US/08664962B
Patent No. 6218162
GENERAL INFORMATION:
APPLICANT: Krystal, Gerald
TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:

ADDRESS: MERCHANT & GOULD
STREET: 3100 NO. 6218162west Center, 90 South Seventh Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: U.S.A.
ZIP: 55402-4131

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,962B
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Douglas P.
REGISTRATION NUMBER: 30,300
REFERENCE/DOCKET NUMBER: MCG 7933.49-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-664-962B-2

Query Match 0.6%; Score 8; DB 3; Length 1185;
Best Local Similarity 100.0%; Pred. No. 1,26+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1075 TLPSLESL 1082
DB 226 TLPSLESL 233

RESULT 35

US-09-311-743-2
Sequence 2, Application US/09311743
Patent No. 6238903
GENERAL INFORMATION:
APPLICANT: Krystal, Gerald
TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESS: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/311,743
FILING DATE: 14-May-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7771-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-364-7311
TELEFAX: 416-361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1185 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-311-743-2

Query Match 0.6%; Score 8; DB 3; Length 1187;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1075 TLPSLESL 1082
Db 226 TLPSLESL 233

RESULT 36
US-08-664-962B-8
Sequence 8, Application US/08664962B
Patent No. 6218162
GENERAL INFORMATION:
APPLICANT: KYREAL, Gerald
TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MERCHANT & GOULD
STREET: 3100 No. 6218162west Center, 90 South Seventh Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: U.S.A.
ZIP: 55402-4131
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,962B
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Douglas P.
REGISTRATION NUMBER: 30,300
REFERENCE/DOCKET NUMBER: M&G 7933.49-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-664-962B-8

Query Match 0.6%; Score 8; DB 3; Length 1187;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1075 TLPSLESL 1082
Db 226 TLPSLESL 233

RESULT 37
US-09-311-743-8
Sequence 8, Application US/09311743
Patent No. 6238903
GENERAL INFORMATION:
APPLICANT: KYREAL, Gerald
TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERNSTEIN & PARR

STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/311,743
FILING DATE: 14-May-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7771-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-364-7311
TELEFAX: 416-361-1398
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-311-743-8

Query Match 0.6%; Score 8; DB 3; Length 1187;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1075 TLPSLESL 1082
Db 226 TLPSLESL 233

RESULT 38
US-09-195-868-15
Sequence 15, Application US/09195868
Patent No. 6090621
GENERAL INFORMATION:
APPLICANT: KAVANAUGH MD, MICHAEL
APPLICANT: POT PH.D., DAVID
TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 HORTON STREET
CITY: EMERYVILLE
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,868
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US/09/195,868
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FIRESTONE, LEIGH H.
REGISTRATION NUMBER: 36,831
REFERENCE/DOCKET NUMBER: 1182.004
TELECOMMUNICATION INFORMATION:

TELEPHONE: 510-923-2707
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-195-868-15

Query Match 0.6%; Score 8; DB 3; Length 1189;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1075 TLPSLESL 1082
|||||
Db 227 TLPSLESL 234

RESULT 39
US-09-195-868-28
Sequence 28, Application US/09195868
Patent No. 6090621
GENERAL INFORMATION:
APPLICANT: KAVANAUGH MD, MICHAEL
APPLICANT: POT PH.D., DAVID
APPLICANT: WILLIAMS MDPH, LEWIS T.
TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE
TITLE OF INVENTION: 5-PHOSPHATASES (SIPS)
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 HORTON STREET
CITY: EMERYVILLE
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,868
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US/09/195,868
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FIRSTONE, LEEGH H.
REGISTRATION NUMBER: 36,831
REFERENCE/DOCKET NUMBER: 1182.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-923-2707
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-195-868-28

Query Match 0.6%; Score 8; DB 3; Length 1229;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1075 TLPSLESL 1082
|||||
Db 267 TLPSLESL 274

RESULT 40
US-09-515-514-15
Sequence 15, Application US/09515514
Patent No. 6509162
GENERAL INFORMATION:
APPLICANT: Alcler, Dario C.
TITLE OF INVENTION: Methods for Selectively Modulating Survival Apoptosis
FILE REFERENCES: 44574-5063-US
CURRENT APPLICATION NUMBER: US/09/515,514
CURRENT FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: NAIP phosphorylation motif
US-09-515-514-15

Query Match 0.5%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 WIPQEMA 82
|||||
Db 1 WIPQEMA 7

RESULT 41
US-08-078-311-9
Sequence 9, Application US/08078311
Patent No. 5925750
GENERAL INFORMATION:
APPLICANT: Charon, Martine
APPLICANT: Gisselbrecht, Sylvie
APPLICANT: Penciolelli, Jean-Francois
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5925750west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/FR90/00762
FILING DATE: 19-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Katherine M.
REGISTRATION/DOCKET NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.84USMO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300

TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-078-311-9

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 LSAALGL 29
Db 11 LSAALGL 17

RESULT 42

US-08-460-402-9
Sequence 9, Application US/08460402
Patent No. 5989833

GENERAL INFORMATION:

APPLICANT: Charon, Martine
APPLICANT: Gieselbrecht, Sylvie
APPLICANT: Benoitelli, Jean-Francois
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchante & Gould
STREET: 90 South 7th Street, 3100 No. 5989833west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460.402
FILING DATE:
CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/109.259
FILING DATE: 20-SEP-1994
CLASSIFICATION: 436
APPLICATION NUMBER: US 08/078.311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: MO PCT/FR90/00762
FILING DATE: 14-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Randall A. Hillson
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.84US03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-402-9

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 LSAALGL 29
Db 11 LSAALGL 17

RESULT 43

US-09-045-632-68
Sequence 68, Application US/09045632
Patent No. 6001575

GENERAL INFORMATION:

APPLICANT: Huganir, Richard L.
APPLICANT: Dong, Hualing
TITLE OF INVENTION: THERAPEUTIC USES OF GRIP AND
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045.632
FILING DATE: 19-MAR-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/041.016
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F.
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 48147/1699-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-045-632-68

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 578 LIAVATN 564
Db 24 LIAVATN 30

RESULT 44

US-08-176-500-71
Sequence 71, Application US/08176500
Patent No. 5498538

GENERAL INFORMATION:

APPLICANT: Kay, B. K.

APPLICANT: Fowlkes, D. M.
 TITLE OF INVENTION: Totally Synthetic Affinity Reagents
 NUMBER OF SEQUENCES: 141
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/176,500
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/013,416
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mierock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-143
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-8864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULAR TYPE: peptide
 US-08-176-500-71

Query Match 0.5%; Score 7; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 941 SOVPTD 947
 DB 1 SOVPTD 7

RESULT 45
 US-08-471-052A-71
 Sequence 71, Application US/08471052A
 Patent No. 5625033
 GENERAL INFORMATION:
 APPLICANT: Kay, B. K.
 APPLICANT: Fowlkes, D. M.
 TITLE OF INVENTION: Totally Synthetic Affinity Reagents
 NUMBER OF SEQUENCES: 166
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,052A
 FILING DATE: 06-JUNE-1995
 CLASSIFICATION: 530

```

ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-052A-71

Query Match          0.5%: Score 7; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          941 SQVPTID 947
|||||
Db          1 SQVPTID 7

RESULT 46
US-08-189-331-71
Sequence 71, Application US/08189331
Patent No. 5747334
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICATOR: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,331
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-189-331-71

Query Match          0.5%: Score 7; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          941 SQVPTID 947
|||||
Db          1 SQVPTID 7

```

Db 1 SQVPTID 7

RESULT 47

US-08-471-939-71

Sequence 71, Application US/08471939

Patent No. 5844076

GENERAL INFORMATION:

APPLICANT: Kay, B. K.

APPLICANT: Fowles, D. M.

TITLE OF INVENTION: Totally Synthetic Affinity Reagents

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,939

FILING DATE: 06-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 530

FILING DATE: 01-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-143

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-471-939-71

Query Match 0.5%; Score 7; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 SQVPTID 7

RESULT 48

US-08-471-800-71

Sequence 71, Application US/08471800

Patent No. 5852167

GENERAL INFORMATION:

APPLICANT: Kay, B. K.

APPLICANT: Fowles, D. M.

TITLE OF INVENTION: Totally Synthetic Affinity Reagents

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,800

FILING DATE: 06-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/013,416

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-143

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-471-800-71

Query Match 0.5%; Score 7; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 SQVPTID 7

RESULT 49

US-08-471-068-71

Sequence 71, Application US/08471068

Patent No. 5948635

GENERAL INFORMATION:

APPLICANT: Kay, B. K.

APPLICANT: Fowles, D. M.

TITLE OF INVENTION: Totally Synthetic Affinity Reagents

NUMBER OF SEQUENCES: 186

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,068

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/169,331

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-155

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741
 TELETYPE: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-471-068-71

Query Match 0.5%; Score 7; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 941 SOVPTID 947
 DB 1 SOVPTID 7

RESULT 50
 US-08-569-749-9
 Sequence 9, Application US/08569749
 Patent No. 6187557

GENERAL INFORMATION:
 APPLICANT: Rotne, Mike
 APPLICANT: Goeddel, David V
 TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/569,749
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Brezner, David J.
 REGISTRATION NUMBER: 24,774
 REFERENCE/DOCKET NUMBER: A-62464/DJB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415)781-1989
 TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 48 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-569-749-9

Query Match 0.5%; Score 7; DB 3; Length 48;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 EHAKEP 222
 DB 39 EHAKEP 45

RESULT 51
 PCT-US96-12860-9
 Sequence 9, Application PC/TUS9612860

GENERAL INFORMATION:
 APPLICANT: TULARIK, INC.
 TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/12860
 FILING DATE: 06 AUG 1996
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Brezner, David J.
 REGISTRATION NUMBER: 24,774
 REFERENCE/DOCKET NUMBER: A-62464/DJB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415)781-1989
 TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 48 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-12860-9

Query Match 0.5%; Score 7; DB 5; Length 48;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 EHAKEP 222
 DB 39 EHAKEP 45

RESULT 52
 US-09-177-249-94
 Sequence 94, Application US/09177249
 Patent No. 6229064

GENERAL INFORMATION:
 APPLICANT: Fischer, Robert L.
 APPLICANT: Ohad, Nir
 APPLICANT: Kiyosue, Tomohiro
 APPLICANT: Yadegari, Ramin
 APPLICANT: Margossian, Linda
 APPLICANT: Harada, John
 APPLICANT: Goldberg, Robert B.
 TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
 FILE REFERENCE: 023070-086120US
 CURRENT APPLICATION NUMBER: US/09/177,249
 EARLIER APPLICATION NUMBER: US 09/071,838
 NUMBER OF SEQ ID NOS: 124
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 94
 LENGTH: 50
 TYPE: PRT

ORGANISM: Arabidopsis sp.
US-09-177-249-94

Query Match

Best Local Similarity 100.0%; Score 7; DB 3; Length 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 621 RLRKFW 627
DB 20 RLKRFV 26

RESULT 53

US-08-975-080-21
Sequence 21, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975.080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
FAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-080-21

Query Match

Best Local Similarity 100.0%; Score 7; DB 3; Length 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 216 EHAKEP 222
DB 29 EHAKEP 35

RESULT 54

US-08-975-080-22
Sequence 22, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975.080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975.080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
FAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-080-22

Query Match

Best Local Similarity 100.0%; Score 7; DB 3; Length 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 216 EHAKEP 222
DB 29 EHAKEP 35

RESULT 55

US-08-975-080-31
Sequence 31, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975.080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988

REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-975-080-31
MOLECULE TYPE: protein

Query Match 0.5%; Score 7; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 EHAKP 222
Db 29 EHAKP 35

RESULT 56
US-08-511-485-23
Sequence 23, Application US/08511485
Patent No. 591912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSES: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELFX: 200154
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-23

Query Match 0.5%; Score 7; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 339 PPNCPFL 345
Db 61 PPNCPFL 67

RESULT 57
US-09-201-936-23
Sequence 23, Application US/09201936
Patent No. 6541457
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-23

Query Match 0.5%; Score 7; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 339 PPNCPFL 345
Db 61 PPNCPFL 67

RESULT 58
US-08-511-485-27
Sequence 27, Application US/08511485
Patent No. 591912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSES: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEFAX: 200154
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 68 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: both
 MOLECULE TYPE: protein
 US-08-511-485-27

Query Match

Best Local Similarity 0.5%; Score 7; DB 2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 EHAKEP 222
 Db 57 EHAKEP 63

RESULT 59

US-09-201-936-27
 Sequence 27, Application US/09201936
 Patent No. 6541457
 GENERAL INFORMATION:
 APPLICANT: Korneluk, Robert G.
 APPLICANT: Mackenzie, Alexander E.
 APPLICANT: Baird, Stephen
 APPLICANT: Lister, Peter
 TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 FILE REFERENCE: PROBES, AND DETECTION METHODS
 CURRENT APPLICATION NUMBER: US/09/201,936
 EARLIER FILING DATE: 1998-12-01
 EARLIER APPLICATION NUMBER: 09/011,356
 EARLIER FILING DATE: 1998-02-04
 EARLIER APPLICATION NUMBER: PCT/1996/01022
 EARLIER FILING DATE: 1996-06-05
 EARLIER APPLICATION NUMBER: 08/576,956
 EARLIER FILING DATE: 1995-12-22
 EARLIER APPLICATION NUMBER: 08/511,485
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO: 27
 LENGTH: 68
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-201-936-27

Query Match

Best Local Similarity 0.5%; Score 7; DB 4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 EHAKEP 222
 Db 57 EHAKEP 63

RESULT 60

US-08-469-412A-14
 Sequence 14, Application US/08469412A
 Patent No. 5656125
 GENERAL INFORMATION:
 APPLICANT: Mavrothalasitis, George J.
 APPLICANT: Blair, Donald G.
 APPLICANT: Fisher, Robert J.
 APPLICANT: Beal Jr., Gregory J.
 APPLICANT: Athanasiou, Meropi A.
 APPLICANT: Sgouras, Dionysios N.
 TITLE OF INVENTION: The ERF Genetic Locus and Its Products
 NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,412A
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Garrett-Mackowski, Eugenia
 REGISTRATION NUMBER: 37,330
 REFERENCE/DOCKET NUMBER: 015280-229000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
 LENGTH: 81 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 1..81
 OTHER INFORMATION:
 OTHER INFORMATION: /note= "Yan homologous region to
 US-08-469-412A-14
 ets-like ERF DNA-binding domain"

Query Match

Best Local Similarity 0.5%; Score 7; DB 2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 567 IOKNLS 573
 Db 44 IOKNLS 50

RESULT 61

US-09-021-715-14
 Sequence 14, Application US/09021715
 Patent No. 6194547
 GENERAL INFORMATION:
 APPLICANT: Mavrothalasitis, George J.
 APPLICANT: Blair, Donald G.
 APPLICANT: Fisher, Robert J.
 APPLICANT: Beal Jr., Gregory J.
 APPLICANT: Sgouras, Dionysios N.
 APPLICANT: Athanasiou, Meropi A.
 TITLE OF INVENTION: The ERF Genetic Locus and Its Products
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/021,715

FILING DATE: 10-Feb-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,350
REFERENCE/DOCKET NUMBER: 015280-229000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Domain
LOCATION: 1..81
OTHER INFORMATION: /note="Yan homologous region to
etc-like ERP DNA-binding domain"
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-021-715-14

Query Match 0.5%; Score 7; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 567 IOKNHLS 573
Db 44 IOKNHLS 50

RESULT 62
US-09-100-804-24
Sequence 24, Application US/09100804
Patent No. 6066472
GENERAL INFORMATION:
APPLICANT: GOMEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLARSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616

REFERENCE/DOCKET NUMBER: 10461/7003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 83 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-100-804-24

Query Match 0.5%; Score 7; DB 3; Length 83;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 578 LIAYRTN 584
Db 48 LIAYRTN 54

RESULT 63
US-09-328-352-5481
Sequence 5481, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5481
LENGTH: 129
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-5481

Query Match 0.5%; Score 7; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 AKRLKTF 67
Db 105 AKRLKTF 111

RESULT 64
US-09-328-352-5532
Sequence 5532, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5532
LENGTH: 139
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-5532

Query Match 0.5%; Score 7; DB 4; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 AKRLKTF 67
Db 105 AKRLKTF 111

RESULT 65
US-09-328-352-5595
Sequence 5595, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5595
LENGTH: 145
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-5595

Query Match
Best Local Similarity 0.5%; Score 7; DB 4; Length 145;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 61 AKRLKTF 67
Db 105 AKRLKTF 111

RESULT 66
US-09-328-352-5394
Sequence 5394, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5394
LENGTH: 152
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-5394

Query Match
Best Local Similarity 0.5%; Score 7; DB 4; Length 152;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 61 AKRLKTF 67
Db 105 AKRLKTF 111

RESULT 67
US-09-738-946-4
Sequence 4, Application US/09738946
Patent No. 6578701
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED IN CANCER
FILE REFERENCE: EX00-043C
CURRENT APPLICATION NUMBER: US/09/738,946
PRIOR FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 60/170,832
PRIOR FILING DATE: 1999-12-14

PRIOR APPLICATION NUMBER: 60/170,838
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: 60/178,580
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/185,879
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 60/185,880
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 60/186,150
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/189,701
PRIOR FILING DATE: 2000-03-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 153
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-738-946-4

Query Match
Best Local Similarity 0.5%; Score 7; DB 4; Length 153;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 211 DDPWKEH 217
Db 84 DDPWKEH 90

RESULT 68
US-09-328-352-7105
Sequence 7105, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7105
LENGTH: 159
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-7105

Query Match
Best Local Similarity 0.5%; Score 7; DB 4; Length 159;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 61 AKRLKTF 67
Db 105 AKRLKTF 111

RESULT 69
US-08-034-245-14
Sequence 14, Application US/08034245
Patent No. 5504197
GENERAL INFORMATION:
APPLICANT: Schubert, David
TITLE OF INVENTION: NEUROTROPIC GROWTH FACTOR AND METHODS
FILE REFERENCE: OF TREATMENT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Prately, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/034,245
FILING DATE: 19930322
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,359
FILING DATE: 27-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/541,276
FILING DATE: 20-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9369
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-034-245-14

Query Match 0.5%; Score 7; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEEOKE 45
|||||
Db 36 EEEEOKE 42

RESULT 70
US-08-078-311-4
Sequence 4, Application US/08078311
Patent No. 5925750
GENERAL INFORMATION:
APPLICANT: Charon, Martine
APPLICANT: Gisselbrecht, Silvie
APPLICANT: Penciolelli, Jean-Francios
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5925750west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: NO PCT/FR90/00762
FILING DATE: 19-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.84USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-078-311-4

Query Match 0.5%; Score 7; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LSAALLGL 29
|||||
Db 56 LSAALLGL 62

RESULT 71
US-08-460-402-4
Sequence 4, Application US/08460402
Patent No. 5989833
GENERAL INFORMATION:
APPLICANT: Charon, Martine
APPLICANT: Gisselbrecht, Silvie
APPLICANT: Penciolelli, Jean-Francios
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5989833west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,402
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,259
FILING DATE: 20-SEP-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 14-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Randall A. Hillson
REGISTRATION NUMBER: 31,838

REFERENCE/DOCKET NUMBER: 8076.84US03
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-332-5300
 TELEFAX: 612-332-5300
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-460-402-4

Query Match
 Best Local Similarity 0.5%; Score 7; DB 2; Length 184;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 23 LSNLGL 29
 56 LSNLGL 62

RESULT 72

US-09-328-352-7240
 Sequence 7240, Application US/09328352
 Patent No. 6562958
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 FILE REFERENCE: CIPC9-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 7240
 LENGTH: 189
 TYPE: PRP
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-7240

Query Match

Best Local Similarity 0.5%; Score 7; DB 4; Length 189;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 AKRLKTF 67
 105 AKRLKTF 111

RESULT 73

US-08-188-582-24
 Sequence 24, Application US/08188582
 Patent No. 5634410
 GENERAL INFORMATION:

APPLICANT: Tjian, Robert
 APPLICANT: Comai, Lucio
 APPLICANT: Dynlacht, Brian D.
 APPLICANT: Hoey, Timothy
 APPLICANT: Rupprecht, Siegfried
 APPLICANT: Tanese, Naoko
 APPLICANT: Wang, Edith
 APPLICANT: Weinzierl, Robert O.J.
 TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESSES:
 ADDRESS: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/188,582
 FILING DATE: 28-JAN-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Osman, Richard A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 197 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-188-582-24

Query Match
 Best Local Similarity 0.5%; Score 7; DB 1; Length 197;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 36 KELEEE 42
 80 KELEEE 86

RESULT 74

US-08-646-715-24
 Sequence 24, Application US/08646715
 Patent No. 5637686
 GENERAL INFORMATION:

APPLICANT: Tjian, Robert
 APPLICANT: Comai, Lucio
 APPLICANT: Dynlacht, Brian D.
 APPLICANT: Hoey, Timothy
 APPLICANT: Rupprecht, Siegfried
 APPLICANT: Tanese, Naoko
 APPLICANT: Wang, Edith
 APPLICANT: Weinzierl, Robert O.J.
 TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESSES:
 ADDRESS: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,715
 FILING DATE: 09-MAY-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Osman, Richard A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989

```

: TELEFAX: (415)398-3249
:
: TELEEX: 910 277299
:
: INFORMATION FOR SEQ ID NO: 24
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 197 amino acids
:
: TYPE: amino acid
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
US-08-646-715-24

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Query Match	0.5%	Score 7;	DB 1;	Length 197;
Best Local Similarity	100.0%	Pred. No. 2.2e+02;		
Matches 7;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	36	KELEEE	42
Db	80	KELEEE	86

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RESULT 75
US-09-134-001C-4407
: Sequence 4407, Application US/09134001C
: Patent No. 6380370
: GENERAL INFORMATION:
: APPLICANT: Lynn Doucette-Stamm et al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
: TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: GTC-007
: CURRENT APPLICATION NUMBER: US/09/134,001C
: CURRENT FILING DATE: 1998-08-13
: PRIOR APPLICATION NUMBER: US 60/064,964
: PRIOR FILING DATE: 1997-11-08
: PRIOR APPLICATION NUMBER: US 60/055,779
: PRIOR FILING DATE: 1997-08-14
: NUMBER OF SEQ ID NOS: 5674
: SEQ ID NO 4407
: LENGTH: 223
: TYPE: PR1
: ORGANISM: Staphylococcus epidermidis
: US-09-134-001C-4407

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Query Match	0.5%	Score 7;	DB 4;	Length 223;
Best Local Similarity	100.0%	Pred. No. 2.4e+02;		
Matches 7;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      618 NMTRLRK 624
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Db      196 NMTRLRK 202
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Search completed: December 18, 2003, 09:16:06
Job time : 27 secs

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OM protein - protein search, using sw model

Run on: December 18, 2003, 09:11:49 ; Search time 76 Seconds
(without alignments)
4763.787 Million cell updates/sec

Title: US-09-830-338-1
Perfect score: 1403
Sequence: 1 MATQKASDERISQFDMHL.....SKYLLIQKWLPPSPRIQK 1403

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database: SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protein:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1099	78.3	1160	4	Q8TND4
2	35	2.5	1271	11	Q8CH71
3	35	2.5	1432	11	Q8CGS9
4	35	2.5	1446	11	Q8CG17
5	35	2.5	1447	11	Q8CH66
6	35	2.5	1447	11	Q8CGT1
7	35	2.5	1447	11	Q8CGT0
8	35	2.5	1447	11	Q8CGS8
9	35	2.5	1447	11	Q8CGS7
10	26	1.9	1402	11	Q8CH65
11	26	1.9	1403	11	Q8CH70
12	24	1.7	597	11	Q9R015
13	24	1.7	1402	11	Q8CGT4
14	24	1.7	1402	11	Q8CGT3
15	24	1.7	1403	11	Q8CH68
16	24	1.7	1403	11	Q8CH64

17	24	1.7	1403	11	Q8CGT2	Q8CGT2 mus musculus
18	24	1.7	1403	11	Q8B658	Q8B658 mus musculus
19	23	1.6	517	11	Q8R4U8	Q8R4U8 rattus norv
20	16	1.1	100	11	Q8CAX8	Q8CAX8 mus musculus
21	21	0.8	87	11	Q8G123	Q8G123 mus musculus
22	22	0.8	87	11	Q8G120	Q8G120 mus musculus
23	10	0.7	87	11	Q8G119	Q8G119 mus musculus
24	9	0.6	210	16	Q9J7PD4	Q9J7PD4 streptococ
25	9	0.6	241	17	Q8TP89	Q8TP89 methanococ
26	9	0.6	349	11	Q8R282	Q8R282 mus musculus
27	9	0.6	349	11	Q8D564	Q8D564 mus musculus
28	9	0.6	349	11	Q8B283	Q8B283 mus musculus
29	9	0.6	350	6	Q9H5K3	Q9H5K3 homo sapien
30	9	0.6	360	4	Q95J00	Q95J00 macaca fasc
31	31	0.6	414	10	Q9LX22	Q9LX22 arabidopsis
32	32	0.6	439	10	Q9FJPD	Q9FJPD arabidopsis
33	33	0.6	469	10	Q8GUK8	Q8GUK8 arabidopsis
34	34	0.6	827	16	Q9H1Y5	Q9H1Y5 pseudomonas
35	35	0.6	74	2	Q9ZHW8	Q9ZHW8 bruceella me
36	36	0.6	111	11	Q9W0H6	Q9W0H6 mus musculus
37	37	0.6	120	1	Q86500	Q86500 desulfuroco
38	38	0.6	146	17	Q9YDD1	Q9YDD1 aeropyrum p
39	39	0.6	147	16	Q9RSR8	Q9RSR8 deinococcus
40	40	0.6	151	5	Q8IR03	Q8IR03 drosophila
41	41	0.6	152	17	Q930299	Q930299 drosophila
42	42	0.6	155	12	Q9YMI9	Q9YMI9 lymantria d
43	43	0.6	169	17	Q8ZU27	Q8ZU27 pyrobaculum
44	44	0.6	192	4	Q9Y329	Q9Y329 homo sapien
45	45	0.6	197	5	Q9VX87	Q9VX87 drosophila
46	46	0.6	202	5	P91724	P91724 drosophila
47	47	0.6	213	5	Q8MWN1	Q8MWN1 bolentina vi
48	48	0.6	219	2	Q52735	Q52735 rhizobium e
49	49	0.6	219	16	Q8UC11	Q8UC11 agrobacteri
50	50	0.6	220	16	Q8XFR2	Q8XFR2 salmonele
51	51	0.6	232	10	Q8LB50	Q8LB50 arabidopsis
52	52	0.6	232	10	Q9LP21	Q9LP21 arabidopsis
53	53	0.6	253	11	Q9Z2B4	Q9Z2B4 rattus norv
54	54	0.6	253	11	Q9QY27	Q9QY27 mus musculus
55	55	0.6	253	11	Q9DD12	Q9DD12 mus musculus
56	56	0.6	268	13	Q9DGN3	Q9DGN3 gallus gall
57	57	0.6	307	16	Q8FLC0	Q8FLC0 escherichia
58	58	0.6	314	2	Q9X6M1	Q9X6M1 escherichia
59	59	0.6	315	16	Q98JF7	Q98JF7 rhizobium l
60	60	0.6	329	5	Q46012	Q46012 caenorhabd
61	61	0.6	331	16	Q8XV61	Q8XV61 raietonia b
62	62	0.6	333	2	Q93E95	Q93E95 enterococcu
63	63	0.6	345	17	Q57896	Q57896 pyrococcus
64	64	0.6	358	10	Q8LB55	Q8LB55 arabidopsis
65	65	0.6	358	10	Q8Z487	Q8Z487 arabidopsis
66	66	0.6	365	16	Q97H79	Q97H79 clostridium
67	67	0.6	372	16	Q9ZNG8	Q9ZNG8 rhizobium m
68	68	0.6	372	16	Q8DTQ0	Q8DTQ0 streptococc
69	69	0.6	390	16	Q98DC3	Q98DC3 rhizobium l
70	70	0.6	391	16	Q54143	Q54143 streptomyce
71	71	0.6	396	5	Q04151	Q04151 toxoplasma
72	72	0.6	401	13	Q8THV9	Q8THV9 xenopus lae
73	73	0.6	422	17	Q9Y106	Q9Y106 pyrococcus
74	74	0.6	429	16	Q98CE6	Q98CE6 rhizobium l
75	75	0.6	437	16	Q98C91	Q98C91 rhizobium l
76	76	0.6	470	2	Q8RNP3	Q8RNP3 legionella
77	77	0.6	489	16	Q8FCZ4	Q8FCZ4 escherichia
78	78	0.6	496	11	Q9ESFO	Q9ESFO rattus norv
79	79	0.6	501	11	Q9B004	Q9B004 rattus norv
80	80	0.6	501	11	Q9B005	Q9B005 rattus norv
81	81	0.6	521	5	Q9VTP9	Q9VTP9 drosophila
82	82	0.6	532	11	Q9QY28	Q9QY28 mus musculus
83	83	0.6	538	5	Q9VGB6	Q9VGB6 drosophila
84	84	0.6	575	5	Q9VGB5	Q9VGB5 drosophila
85	85	0.6	654	10	Q9ZTW9	Q9ZTW9 oryza sativ
86	86	0.6	656	10	Q9ZTX2	Q9ZTX2 ipomoea bat
87	87	0.6	657	10	Q94C06	Q94C06 ipomoea bat
88	88	0.6	671	4	Q95559	Q95559 homo sapien
89	89	0.6	679	5	Q9VJ15	Q9VJ15 drosophila

90	8	0.6	679	5	Q24185
91	8	0.6	682	10	Q94C08
92	8	0.6	803	16	Q98185
93	8	0.6	837	11	Q63618
94	8	0.6	840	10	Q81PM3
95	8	0.6	845	4	Q9Y4Q0
96	8	0.6	854	4	Q9Y4Q0
97	8	0.6	871	11	Q9ET47
98	8	0.6	926	10	Q8L8N0
99	8	0.6	934	10	Q81080
100	8	0.6	959	11	Q9UKR7

ALIGNMENTS

RESULT 1

08TDZ4 PRELIMINARY; PRT: 1160 AA.

AC 08TDZ4; TREMBLrel. 21, Created;
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Pei neuronal apoptosis inhibitory protein (Fragment).
 GN PSINAIIP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_Textid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xu M., Okada T., Sakai H., Miyamoto N., Yanagisawa Y., MacKenzie A.E.,
 RA "Functional human NAIP promoter and transcriptional regulatory
 RT element for the human NAIP and psinaiip genes."
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBD databases.
 DR EMBL: AB048534; BAB87181.1;
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR001370; BIR-
 DR InterPro: IPR007111; NACHT_NTPase.
 DR Pfam: PF00653; BIR_1.
 DR SMART: SM00382; AAA_1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 1.
 DR PROSITE: PS01443; BIR_REPEAT_2; 1.
 DR PROSITE: PS00837; NACHT_1.
 KW ATP-binding; NACHT; 1.
 FT NON TER
 SQ SEQUENCE 1160 AA; 131893 MW; 78C947C93AA4F5876 CRC64;

Query Match 78.3%; Score 1099; DB 4; Length 1160;
 Matches 1099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	224	CEPLRSKSSSEIT	YIOSYKGPVDITGSHFNVSVORELPMASAYCNSDIFAYEELRD	283
DB	62	CEPLRSKSSSEIT	YIOSYKGPVDITGSHFNVSVORELPMASAYCNSDIFAYEELRD	121
QY	284	SFKDMPRESAV	AVNAALAKGLFTYTGKIDIVQCFSCGGLCKEMOGDDPLDDHTRCFPNCP	343
DB	122	SFKDMPRESAV	AVNAALAKGLFTYTGKIDIVQCFSCGGLCKEMOGDDPLDDHTRCFPNCP	181
QY	344	FLONKSSAEV	TPDLSRGELCELLTSSSENLDSIAYNPVPEMAQCEAMFOEAKNL	403
DB	182	FLONKSSAEV	TPDLSRGELCELLTSSSENLDSIAYNPVPEMAQCEAMFOEAKNL	241
QY	404	NEQIRAAV	YTSAPFRHSLDISSDATDHLGCLSLASGHLSKVPQPLVPEVGNLN	463
DB	242	NEQIRAAV	YTSAPFRHSLDISSDATDHLGCLSLASGHLSKVPQPLVPEVGNLN	301
QY	464	SVNCEGASG	CKTVLLKKIAFIAMAGCCPLNRFOLVYLSLSTRDEGLASIIICDL	523
DB	302	SVNCEGASG	CKTVLLKKIAFIAMAGCCPLNRFOLVYLSLSTRDEGLASIIICDL	361

QY	524	LEKGSVTECM	GNITIQOLKNQVFLDDYVKEICSIPOVYIGLQIKHLSRTCLLAVRT	583
DB	362	LEKGSVTECM	GNITIQOLKNQVFLDDYVKEICSIPOVYIGLQIKHLSRTCLLAVRT	421
QY	584	NRADIRRL	YLETITLEIKAPFPYNTVCILRLPFHNMTRLRKMTYEGKNSLOKIQTP	643
DB	422	NRADIRRL	YLETITLEIKAPFPYNTVCILRLPFHNMTRLRKMTYEGKNSLOKIQTP	481
QY	644	FVAICAHW	QYPPDPSPFDVAAPKSYMERLSLRKQATLITAKTVSSCGELAKGFSC	703
DB	482	FVAICAHW	QYPPDPSPFDVAAPKSYMERLSLRKQATLITAKTVSSCGELAKGFSC	541
QY	704	CFEFND	DLAAGVDEDEDITMCLMSKFTAGRLPPYRFLSPAFQSLGMLIELSD	763
DB	542	CFEFND	DLAAGVDEDEDITMCLMSKFTAGRLPPYRFLSPAFQSLGMLIELSD	601
QY	764	ROEHOD	GLYHLKQINSPPMTVSAYNNFANVSSLPSTKGPRIYSHLHLVDNKSLEN	823
DB	602	ROEHOD	GLYHLKQINSPPMTVSAYNNFANVSSLPSTKGPRIYSHLHLVDNKSLEN	661
QY	824	ISENDY	LKIQPEISLQMLRGLMQICPOAYSPMSBHLVALAKTAYQSNVAAACSP	883
DB	662	ISENDY	LKIQPEISLQMLRGLMQICPOAYSPMSBHLVALAKTAYQSNVAAACSP	721
QY	884	VLOFLQ	RTLTGALNLQYFPDPHESLSLRSTHPIRGNKTSPPRAPSYLETCFDSQV	943
DB	722	VLOFLQ	RTLTGALNLQYFPDPHESLSLRSTHPIRGNKTSPPRAPSYLETCFDSQV	781
QY	944	PTIDDY	ASAPFPMNEMERNLAEKEDVNSYMDOMRASPDLSTGYKMLPKQYKIPCE	1003
DB	782	PTIDDY	ASAPFPMNEMERNLAEKEDVNSYMDOMRASPDLSTGYKMLPKQYKIPCE	841
QY	1004	VDVND	DDVQGMELMTYTPASQRIELHLNHSRGPESIRPPLBELSKVATKCSISKL	1063
DB	842	VDVND	DDVQGMELMTYTPASQRIELHLNHSRGPESIRPPLBELSKVATKCSISKL	901
QY	1064	ELSAE	QELTLTLPSELSLEVSGTIOQDOQIPNIDFLCLKLSLVDLGNINVSIVPE	1123
DB	902	ELSAE	QELTLTLPSELSLEVSGTIOQDOQIPNIDFLCLKLSLVDLGNINVSIVPE	961
QY	1124	BFPNFH	HEKLLIQISAEYDPSKLVKLQNSPMLHVFHKLKNFSDFGSLMTMLVSCKL	1183
DB	962	BFPNFH	HEKLLIQISAEYDPSKLVKLQNSPMLHVFHKLKNFSDFGSLMTMLVSCKL	1021
QY	1184	TEIKFS	DPFOAVPFAVSLPNISLKLNLKLNLEGOQFPDEBTSEKFAVIIGSLSNLELILP	1243
DB	1022	TEIKFS	DPFOAVPFAVSLPNISLKLNLKLNLEGOQFPDEBTSEKFAVIIGSLSNLELILP	1081
QY	1244	TGQDI	YRVAKLIIQCCQHLRLVLSFFKTLNDSVETAKVATSGSGOKLENLKLISNH	1303
DB	1082	TGQDI	YRVAKLIIQCCQHLRLVLSFFKTLNDSVETAKVATSGSGOKLENLKLISNH	1141
QY	1304	KITEG	YRNFQALDNMPN 1322	
DB	1142	KITEG	YRNFQALDNMPN 1160	

RESULT 2

08CH71 PRELIMINARY; PRT: 1271 AA.

AC 08CH71; TREMBLrel. 23, Created;
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Baculoviral IAP repeat-containing 1b (Fragment).
 GN BIRC1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Textid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.


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RC STRAIN-A/J;
RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,
RA Endritz M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,
RA Dietrich W.F.;
RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
RT Legionella pneumophila.";
RT Curr. Biol. 0:0-0(2003).
DR EMBL: AF367966; AAAT7615.1; JOINED.
DR EMBL: AF367966; AAAT7615.1; JOINED.
PT NON TER 1271 1271
SQ SEQUENCE 1271 AA; 144021 MW; 78213AEC741CBE CRC64;

Query Match 2.5%; Score 35; DB 11; Length 1271;
Best Local Similarity 100.0%; Pred. No. 6e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOFCGCGCLGNWEGDDPMKEHAKMPKCEFL 227
Db 193 DTVOFCGCGCLGNWEGDDPMKEHAKMPKCEFL 227

RESULT 3
08CGS9 PRELIMINARY; PRT; 1432 AA.
AC 08CGS9;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Neuronal apoptosis inhibitory protein 2 (Fragment).
BI RC1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/cJ;
RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,
RA Endritz M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,
RA Dietrich W.F.;
RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
RT Legionella pneumophila.";
RT Curr. Biol. 0:0-0(2003).
DR EMBL: AY147002; AAAT7586.1; -.
FT NON TER 1 1
SQ SEQUENCE 1432 AA; 162454 MW; 55DBE61FD6DE7FD CRC64;

Query Match 2.5%; Score 35; DB 11; Length 1432;
Best Local Similarity 100.0%; Pred. No. 6.7e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOFCGCGCLGNWEGDDPMKEHAKMPKCEFL 227
Db 178 DTVOFCGCGCLGNWEGDDPMKEHAKMPKCEFL 212

RESULT 4
08CG17 PRELIMINARY; PRT; 1446 AA.
ID 08CG17;
AC 08CG17;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Neuronal apoptosis inhibitory protein 2.
GN NAIP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J;
RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,
RA Endritz M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,

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RA Dietrich W.F.;
RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
RT Legionella pneumophila.";
RT Curr. Biol. 0:0-0(2003).
DR EMBL: AF367967; AAAT7615.1; -.
DR EMBL: AF367969; AAAT7615.1; JOINED.
DR EMBL: AF367968; AAAT7615.1; JOINED.
SQ SEQUENCE 1446 AA; 164012 MW; D566E810AF0B0A33 CRC64;

Query Match 2.5%; Score 35; DB 11; Length 1446;
Best Local Similarity 100.0%; Pred. No. 6.7e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOFCGCGCLGNWEGDDPMKEHAKMPKCEFL 227
Db 193 DTVOFCGCGCLGNWEGDDPMKEHAKMPKCEFL 227

RESULT 5
08CH66 PRELIMINARY; PRT; 1447 AA.
ID 08CH66;
AC 08CH66;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE BIRC1B protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/J; TISSUE=Spleen;
RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,
RA Endritz M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,
RA Dietrich W.F.;
RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
RT Legionella pneumophila.";
RT Curr. Biol. 0:0-0(2003).
DR EMBL: AF381710; AAAT7911.1; -.
SQ SEQUENCE 1447 AA; 163998 MW; 0EC3C0B7396E4298 CRC64;

Query Match 2.5%; Score 35; DB 11; Length 1447;
Best Local Similarity 100.0%; Pred. No. 6.7e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOFCGCGCLGNWEGDDPMKEHAKMPKCEFL 227
Db 193 DTVOFCGCGCLGNWEGDDPMKEHAKMPKCEFL 227

RESULT 6
08CGT1 PRELIMINARY; PRT; 1447 AA.
ID 08CGT1;
AC 08CGT1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Neuronal apoptosis inhibitory protein 2.
GN BIRC1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-I29S1;
RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,
RA Endritz M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,
RA Dietrich W.F.;
RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
RT Legionella pneumophila.";
RT Curr. Biol. 0:0-0(2003).

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DR EMBL: AY147001; AAN75584.1; -
SQ SEQUENCE 1447 AA; 16406 MW; SEC27AA27169E02 CRC64;

Query Match 2.5%; Score 35; DB 11; Length 1447;
Best Local Similarity 100.0%; Pred. No. 6.7e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKWPKCEFL 227
Db 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKWPKCEFL 227

RESULT 7

08CGT0 PRELIMINARY; PRT; 1447 AA.
AC 08CGT0
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Neuronal apoptosis inhibitory protein 2.
GN BIRC1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,
RA Endrizzi M.G., Long E.M., Sadigh K., Ahney A.L., Bernstein-Hanley I.,
RA Dietrich W.F.;
RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
Legionella pneumophila.";
RL Curr. Biol. 0:0-0(2003).
DR EMBL: AY147001; AAN75585.1; -
SQ SEQUENCE 1447 AA; 16406 MW; 8C44045962A2F54B CRC64;

Query Match 2.5%; Score 35; DB 11; Length 1447;
Best Local Similarity 100.0%; Pred. No. 6.7e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKWPKCEFL 227
Db 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKWPKCEFL 227

RESULT 8

08CGS8 PRELIMINARY; PRT; 1447 AA.
AC 08CGS8
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Neuronal apoptosis inhibitory protein 2.
GN BIRC1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ;
RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,
RA Endrizzi M.G., Long E.M., Sadigh K., Ahney A.L., Bernstein-Hanley I.,
RA Dietrich W.F.;
RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
Legionella pneumophila.";
RL Curr. Biol. 0:0-0(2003).
DR EMBL: AY147003; AAN75587.1; -
SQ SEQUENCE 1447 AA; 16410 MW; 4BP1679BJF582CF9 CRC64;

Query Match 2.5%; Score 35; DB 11; Length 1447;
Best Local Similarity 100.0%; Pred. No. 6.7e-26;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKWPKCEFL 227
Db 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKWPKCEFL 227

RESULT 9

08CGS7 PRELIMINARY; PRT; 1447 AA.
AC 08CGS7
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Neuronal apoptosis inhibitory protein 2.
GN BIRC1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PVR/N;
RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,
RA Endrizzi M.G., Long E.M., Sadigh K., Ahney A.L., Bernstein-Hanley I.,
RA Dietrich W.F.;
RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
Legionella pneumophila.";
RL Curr. Biol. 0:0-0(2003).
DR EMBL: AY147004; AAN75588.1; -
SQ SEQUENCE 1447 AA; 16410 MW; F5489BCA5EBDD CRC64;

Query Match 2.5%; Score 35; DB 11; Length 1447;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKWPKCEFL 227
Db 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKWPKCEFL 227

RESULT 10

08CH65 PRELIMINARY; PRT; 1402 AA.
AC 08CH65
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE BIRC1B protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J; Tissue=Spleen;
RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,
RA Endrizzi M.G., Long E.M., Sadigh K., Ahney A.L., Bernstein-Hanley I.,
RA Dietrich W.F.;
RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
Legionella pneumophila.";
RL Curr. Biol. 0:0-0(2003).
DR EMBL: AF381771; AAN77912.1; -
SQ SEQUENCE 1402 AA; 159678 MW; 0BA0855BF40B55FD CRC64;

Query Match 1.9%; Score 26; DB 11; Length 1402;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 483 IAFIWMASGCCPLINRFQVLYSLSS 508
Db 483 IAFIWMASGCCPLINRFQVLYSLSS 508

RESULT 11

08CH70 PRELIMINARY; PRT; 1403 AA.
 AC 08CH70;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Baculoviral IAP repeat-containing 1e.
 GN BIRCLIE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A.7;
 RA Wright E.K., Jr., Goodart S.A., Growney J.D., Hadinoto V.,
 RA Endritz M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,
 RA Dietrich W.F.;
 RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
 Legionella pneumophila."
 RL Curr. Biol. 0:0-0(2003).
 DR EMBL: AF367966; AAN7612.1;
 SQ SEQUENCE 1403 AA; 159748 MW; 3237E1CE2BA406EF CRC64;

Query Match 1.9%; Score 26; DB 11; Length 1403;
 Best Local Similarity 100.0%; Pred. No. 1.1e-16;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 483 IAFMWASGCCPLNRFQLVFVYLSLS 508
 Db 483 IAFMWASGCCPLNRFQLVFVYLSLS 508

RESULT 12

09R015 PRELIMINARY; PRT; 597 AA.
 ID 09R015;
 AC 09R015;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Neuronal apoptosis inhibitory protein.
 GN BIRCLIE OR NAIP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99431676; PubMed=10501978;
 RA Huang S., Scharf J.M., Growney J.D., Endritz M.G., Dietrich W.F.;
 RT "The mouse naip gene cluster on chromosome 13 encodes several distinct
 functional transcripts."
 RL Mamm. Genome 10:1032-1035(1999).
 DR EMBL: AF135493; AAD56765.1;
 DR HSSP: Q13490; 1QBH.
 DR MGD: MGI:1298220; Bircle.
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR003892; CUE.
 DR Pfam: PF00653; BIR; 3.
 DR Pfam: PF02845; CUE; 1.
 DR SMART: SM00238; BIR; 3.
 DR PROSITE: PS01282; BIR_REPEAT_2; 3.
 DR PROSITE: PS01433; BIR_REPEAT_2; 3.
 SQ SEQUENCE 597 AA; 68322 MW; 4042E36E51A7F9A0 CRC64;

Query Match 1.7%; Score 24; DB 11; Length 597;
 Best Local Similarity 100.0%; Pred. No. 5.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 204 LGNMBEGDDPWKEHAKWPKCEFL 227
 |||

Db 158 LGNMBEGDDPWKEHAKWPKCEFL 181

RESULT 13

08CGT4 PRELIMINARY; PRT; 1402 AA.
 ID 08CGT4;
 AC 08CGT4;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Neuronal apoptosis inhibitory protein 5.
 GN BIRCLIE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129S1;
 RA Wright E.K., Jr., Goodart S.A., Growney J.D., Hadinoto V.,
 RA Endritz M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,
 RA Dietrich W.F.;
 RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
 Legionella pneumophila."
 RL Curr. Biol. 0:0-0(2003).
 DR EMBL: AF146994; AAN60206.1;
 SQ SEQUENCE 1402 AA; 159584 MW; E8B6C6CA3BF5F372 CRC64;

Query Match 1.7%; Score 24; DB 11; Length 1402;
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 204 LGNMBEGDDPWKEHAKWPKCEFL 227
 |||

Db 204 LGNMBEGDDPWKEHAKWPKCEFL 227

RESULT 14

08CGT3 PRELIMINARY; PRT; 1402 AA.
 ID 08CGT3;
 AC 08CGT3;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Neuronal apoptosis inhibitory protein 5.
 GN BIRCLIE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Wright E.K., Jr., Goodart S.A., Growney J.D., Hadinoto V.,
 RA Endritz M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,
 RA Dietrich W.F.;
 RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
 Legionella pneumophila."
 RL Curr. Biol. 0:0-0(2003).
 DR EMBL: AY146995; AAN60207.1;
 SQ SEQUENCE 1402 AA; 159768 MW; A04C5D45F4B3392 CRC64;

Query Match 1.7%; Score 24; DB 11; Length 1402;
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 204 LGNMBEGDDPWKEHAKWPKCEFL 227
 |||

Db 204 LGNMBEGDDPWKEHAKWPKCEFL 227

RESULT 15
 08CH68

ID 08CH68 PRELIMINARY; PRT; 1403 AA.
 AC 08CH68;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE Neutrol apoptosis inhibitory protein 6.
 GN NAIP6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Wright E.K., Jr., Goodart S.A., Growney J.D., Hadinoto V.,
 RA Dietrich M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,
 RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
 RT Legionella pneumophila.";
 RL Curr. Biol. 0:0-0(2003).
 DR EMBL; AF267969; AAN7617.1;
 SQ SEQUENCE 1403 AA; 159865 MW; AEFEL450334FCCE7 CRC64;
 Query Match
 Best Local Similarity 1.7%; Score 24; DB 11; Length 1403;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 204 LGNMBEGDDPWKEHAKWPKCEFL 227
 Db 204 LGNMBEGDDPWKEHAKWPKCEFL 227

RESULT 16
 ID 08CH64 PRELIMINARY; PRT; 1403 AA.
 AC 08CH64;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE Birc1p protein.
 GN Birc1p.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/J; TISSUE=Spleen;
 RA Wright E.K., Jr., Goodart S.A., Growney J.D., Hadinoto V.,
 RA Dietrich M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,
 RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
 RT Legionella pneumophila.";
 RL Curr. Biol. 0:0-0(2003).
 DR EMBL; AF381772; AAN77913.1;
 SQ SEQUENCE 1403 AA; 159840 MW; 762C19EART10A37A CRC64;
 Query Match
 Best Local Similarity 1.7%; Score 24; DB 11; Length 1403;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 204 LGNMBEGDDPWKEHAKWPKCEFL 227
 Db 204 LGNMBEGDDPWKEHAKWPKCEFL 227

RESULT 17
 ID 08CGT2 PRELIMINARY; PRT; 1403 AA.
 AC 08CGT2;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE Neutrol apoptosis inhibitory protein 5.
 GN NAIP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

GN BIRC1E.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P/J;
 RA Wright E.K., Jr., Goodart S.A., Growney J.D., Hadinoto V.,
 RA Dietrich M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,
 RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
 RT Legionella pneumophila.";
 RL Curr. Biol. 0:0-0(2003).
 DR EMBL; AY146997; AAN60208.1;
 SQ SEQUENCE 1403 AA; 159838 MW; 04C04877908103EE CRC64;
 Query Match
 Best Local Similarity 1.7%; Score 24; DB 11; Length 1403;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 204 LGNMBEGDDPWKEHAKWPKCEFL 227
 Db 204 LGNMBEGDDPWKEHAKWPKCEFL 227

RESULT 18
 ID 08BG68 PRELIMINARY; PRT; 1403 AA.
 AC 08BG68;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE Birc1p protein.
 GN Birc1p.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA16/CJ, C3H/HeJ, and FVB/N;
 RA Wright E.K., Jr., Goodart S.A., Growney J.D., Hadinoto V.,
 RA Dietrich M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,
 RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen
 RT Legionella pneumophila.";
 RL Curr. Biol. 0:0-0(2003).
 DR EMBL; AY146997; AAN60208.1;
 DR EMBL; AY146998; AAN60210.1;
 SQ SEQUENCE 1403 AA; 159816 MW; BD08813D167BBF64 CRC64;
 Query Match
 Best Local Similarity 1.7%; Score 24; DB 11; Length 1403;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 204 LGNMBEGDDPWKEHAKWPKCEFL 227
 Db 204 LGNMBEGDDPWKEHAKWPKCEFL 227

RESULT 19
 ID 08R408 PRELIMINARY; PRT; 517 AA.
 AC 08R408;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DE Neutrol apoptosis inhibitory protein (Fragment).
 GN NAIP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Shin S.W., Park J.W., Lee M.Y., Yoo M., Kim S.K., Oh T.H., Choe B.K.;
RT "Molecular Cloning and Expression of Rat Neuronal Apoptosis Inhibitory
  Protein (NAIP).";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF361881; AAL9667.1; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR007111; NACHT_NTPase.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
DR PROSITE; PS50837; NACHT; 1.
FT NON_TER
FT 517
FT 517
SQ SEQUENCE 517 AA; 58066 MW; 7BD2F80A2037D9C2 CRC64;

Query Match
Best Local Similarity 1.6%; Score 23; DB 11; Length 517;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 AFTWAGCCCLNRFQIVFYL 506
Db 268 AFTWAGCCCLNRFQIVFYL 290

RESULT 20
OCBAX8 PRELIMINARY; PRT; 100 AA.
AC OCBAX8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Baculoviral IAP repeat-containing 1e (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; Pubmed=2466851;
RA THE PANTON Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
  60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK037418; BAC29803.1; -.
FT NON_TER
FT 1
SQ SEQUENCE 100 AA; 11681 MW; 621A21C7542ECF8 CRC64;

Query Match
Best Local Similarity 1.1%; Score 16; DB 11; Length 100;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1304 KITEGYRNFFQALDN 1319
Db 1 KITEGYRNFFQALDN 16

RESULT 21
OCB123 PRELIMINARY; PRT; 87 AA.
AC OCB123;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE BACULOVIRAL IAP repeat-containing protein 1c (Neuronal apoptosis
  inhibitory protein, related sequence 5) (Fragment).

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GN BIRC1C OR NAIP3 OR NAIP-RS5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=97131520; Pubmed=8975718;
RA Schaff J.M., Danton D., Frieella A., Bruno S., Beggs A.H.,
RA Kunzel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
  within the Igml critical interval and contains multiple copies of Naip
  exon 5.";
RL Genomics 38:405-417(1996).
CC -1 SIMILARITY: CONTAINS 1 BIR DOMAIN (BACULOVIRAL INHIBITION OF
  APOPTOSIS PROTEIN REPEAT).
DR EMBL; U66328; AAC52976.1; -.
DR HSSP; Q13490; 10BH.
DR MGD; MGI:1298221; Birc1c.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; PARTIAL.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
FT NON_TER
FT 87
FT 87
SQ SEQUENCE 87 AA; 9997 MW; B184943B1BC52E3A CRC64;

Query Match
Best Local Similarity 0.8%; Score 11; DB 11; Length 87;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 QCFCCSLILFG 106
Db 15 QCFCCSLILFG 25

RESULT 22
OCB120 PRELIMINARY; PRT; 87 AA.
AC OCB120;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE BACULOVIRAL IAP repeat-containing protein 1d (Neuronal apoptosis
  inhibitory protein, related sequence 2) (Fragment).
GN Birc1d OR NAIP4 OR NAIP-RS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=97131520; Pubmed=8975718;
RA Schaff J.M., Danton D., Frieella A., Bruno S., Beggs A.H.,
RA Kunzel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
  within the Igml critical interval and contains multiple copies of Naip
  exon 5.";
RL Genomics 38:405-417(1996).
CC -1 SIMILARITY: CONTAINS 1 BIR DOMAIN (BACULOVIRAL INHIBITION OF
  APOPTOSIS PROTEIN REPEAT).
DR EMBL; U66325; AAC52973.1; -.
DR HSSP; Q13490; 10BH.
DR MGD; MGI:1298221; Birc1d.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; PARTIAL.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
FT NON_TER
FT 1
FT 1

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FT      NON TER      87      87
SQ      SEQUENCE      87 AA; 9972 MW; 9C34CD8224E71325 CRC64;

Query Match
Best Local Similarity 0.8%; Score 11; DB 11; Length 87;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      96 QCFCCSLILF 106
DB      15 QCFCCSLILF 25

RESULT 23
O09119
ID      009119      PRELIMINARY; PRT; 87 AA.
AC      Q09119;
DT      01-JUL-1997 (TrEMBLrel. 04, Created)
DR      01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE      Neutonal apoptosis inhibitory protein related sequence 1
DB      (Fragment)
GN      Birc1-RS1 OR NAIIP-RS1.
OS      Mus musculus (mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      STRAIN=129/SvJ;
RX      MEDLINE=97131520; PubMed=8975718;
RA      Kunkel L.M., Dietrich W.F.;
RT      "The mouse region syntenic for human spinal muscular atrophy lies
RT      within the 1qg1 critical interval and contains multiple copies of Nalp
RT      exon 5."
RL      Genomics 38:405-417(1996).
DR      EMBL; U66324; AAC5972.1; -.
DR      HSSP; Q13490; 10BH.
DR      MGD; MGI:108438; Birc1-RS1.
DR      InterPro: IPR001370; BIR.
DR      Pfam; PF00653; BIR; 1.
DR      SMART; SM00238; BIR; 1.
DR      PROSITE; P550143; BIR_REPEAT_2; 1.
FT      NON TER      87
FT      NON TER      87
SO      SEQUENCE 87 AA; 9958 MW; E601604230BCID25 CRC64;

Query Match
Best Local Similarity 0.7%; Score 10; DB 11; Length 87;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      96 QCFCCSLILF 105
DB      15 QCFCCSLILF 24

RESULT 24
O097PD4
ID      Q097PD4      PRELIMINARY; PRT; 210 AA.
AC      Q097PD4;
DT      01-OCT-2001 (TrEMBLrel. 18, Created)
DR      01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE      ABC transporter, ATP-binding protein.
GN      SP1704.
OS      Streptococcus pneumoniae.
OC      Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX      Streptococcus.
RN      NCB1_TaxID=1113;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=TIGR4;
RX      MEDLINE=21357209; PubMed=11463916;

FT      NON TER      87
FT      NON TER      87
SO      SEQUENCE 87 AA; 9958 MW; E601604230BCID25 CRC64;

Query Match
Best Local Similarity 0.6%; Score 9; DB 16; Length 210;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      473 GSGKTVLTK 481
DB      38 GSGKTVLTK 46

RESULT 25
O08TP89
ID      Q08TP89      PRELIMINARY; PRT; 241 AA.
AC      Q08TP89;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DR      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE      Predicted protein.
GN      MA2025.
OS      Methanosarcina acetivorans.
OC      Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OX      Methanosarcinaceae; Methanosarcina.
RN      NCB1_TaxID=2214;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=C2A / ATCC 35395 / DSM 2834;
RX      MEDLINE=21929760; PubMed=1932238;
RA      Galeagan J.E., Nussbaum C.,
RA      Fitzhugh W., Calvo S., Roy A., Endrizzi M.G., MacDonald P.,
RA      Linton L., McGowan P., McKernan K., Deatellano K., Johnson R.,
RA      Zimmer A., Barber R.D., Cann I., Graham D.E., Tyrrell A., Ye W.,
RA      Heiderich R., Ingram-Smith C., Kuetner H.C., Kizycki J.A.,
RA      Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA      Springer T.A., Uneyama L.A., White O., White R.H., de Macario B.C.,
RA      Ferry J.G., Barrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA      Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA      Metcalf W.W., Birren B.;
RT      "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT      and physiological diversity."
RL      Genome Res. 12:532-542(2002).
DR      EMBL; AB010888; AM05426.1; -.
KW      Complete proteome.
SO      SEQUENCE 241 AA; 27588 MW; 0BB9051BD3B37201 CRC64;

Query Match
Best Local Similarity 0.6%; Score 9; DB 17; Length 241;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      815 VDKKSLN 823
DB      165 VDKKSLN 173

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RESULT 26
OBR252      PRELIMINARY;      PRT;      349 AA.
ID  OBR252;
AC  OBR252;
DT  01-JUN-2002 (TReMBLrel. 21, Created)
DT  01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT  01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE  RIKEN cDNA 493044A02 gene.
GN  493044A02R1K.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RA  SEQUENCE FROM N.A.
RP  Strausberg R.
RL  Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; BC027296; AAt7296.1; -.
DR  MGD; MGI:1921903; 493044A02R1K.
DR  InterPro; IPR000719; Prot_Kinase.
DR  ProDom; PD000001; Prot_Kinase; 1.
DR  PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW  ATP-binding; Transferase.
SQ
SEQUENCE 349 AA; 39982 MW; 527DEB101DB2E12 CRC64;

Query Match      0.6%; Score 9; DB 11; Length 349;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1231 LGSLSNLEE 1239
Db  153 LGSLSNLEE 161

RESULT 27
OBR254      PRELIMINARY;      PRT;      349 AA.
ID  OBR254;
AC  OBR254;
DT  01-JUN-2001 (TReMBLrel. 17, Created)
DT  01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT  01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE  493044A02R1K protein (Hypothetical eukaryotic protein kinase
DE  containing protein).
GN  493044A02R1K.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RA  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=Testis;
RC  MEDLINE=21085660; PubMed=11217851;
RX  Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA  Aikawa T., Hara A., Fukunishi Y., Konno H., Aochi J., Fukuda S.,
RA  Saito T., Okazaki Y., Gojibori T., Bono H., Kaekawa T., Saito R.,
RA  Kato K., Matsuda H.A., Ashburner M., Batcatov S., Caavaant T.,
RA  Fleischmann W., Gaasterland T., Giesi C., King B., Kochwa H.,
RA  Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA  Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Maehio T.,
RA  Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA  Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA  Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA  Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
RA  Lyons P., Marchionni L., Maehima U., Mazzarelli J., Momberters P.,
RA  Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA  Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA  Sasaki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
RA  Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA  Hasegawa Y., Kawaji H., Kohlsuki S.,
RA  "Functional annotation of a full-length mouse cDNA collection.";
RT  Nature 409:685-690(2001).
RN  [2]

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RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=Cerebellum, and Cortex;
RX  MEDLINE=22354683; PubMed=12466851;
RA  The PANTOM Consortium,
RA  the RIKEN Genome Exploration Research Group Phase I & II Team;
RT  "Analysis of the mouse transcriptome based on functional annotation of
RT  60,770 full-length cDNAs.";
RL  Nature 420:563-573(2002).
DR  EMBL; AK015174; BAB29817.1; -.
DR  EMBL; AK012677; BAC27984.1; -.
DR  EMBL; AK043620; BAC31598.1; -.
DR  MGD; MGI:1921903; 493044A02R1K.
DR  InterPro; IPR000719; Prot_Kinase.
DR  Pfam; PF00069; Kinase; 1.
DR  ProDom; PD000001; Prot_Kinase; 1.
DR  PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW  Hypothetical protein; ATP-binding; Transferase.
SQ
SEQUENCE 349 AA; 39968 MW; 0B8683A6D5A95C3 CRC64;

Query Match      0.6%; Score 9; DB 11; Length 349;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1231 LGSLSNLEE 1239
Db  153 LGSLSNLEE 161

RESULT 28
OBR283      PRELIMINARY;      PRT;      349 AA.
ID  OBR283;
AC  OBR283;
DT  01-MAR-2003 (TReMBLrel. 23, Created)
DT  01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT  01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE  Hypothetical eukaryotic protein kinase containing protein.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RA  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=Cerebellum;
RC  MEDLINE=22354683; PubMed=12466851;
RX  The PANTOM Consortium,
RA  the RIKEN Genome Exploration Research Group Phase I & II Team;
RT  "Analysis of the mouse transcriptome based on functional annotation of
RT  60,770 full-length cDNAs.";
RL  Nature 420:563-573(2002).
DR  EMBL; AK036348; BAC29393.1; -.
KW  Hypothetical protein.
SQ
SEQUENCE 349 AA; 39995 MW; FF2C9207C5EB02BD CRC64;

Query Match      0.6%; Score 9; DB 11; Length 349;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1231 LGSLSNLEE 1239
Db  153 LGSLSNLEE 161

RESULT 29
OBR5K3      PRELIMINARY;      PRT;      350 AA.
ID  OBR5K3;
AC  OBR5K3;
DT  01-MAR-2001 (TReMBLrel. 16, Created)
DT  01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT  01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE  Hypothetical protein FLJ23356.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN  [2]

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OX NCBI_TaxID=9606;
RN [1]
RA SEQUENCE FROM N.A.
RA Kawabata A., Hixji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Oka T., Suzuki Y., Odayashi N., Isegai T., Sugano S.,
RT "MEDO human cDNA sequencing project",
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL, AK027009; BAB15623.1;
DR InterPro; IPR000719; Prot kinase.
DR Pfam; PF00069; Kinase; 1_kinase.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KV Hypothetical protein: ATP-binding; transferase.
SQ SEQUENCE 350 AA; 40050 MW; E074FDB2E5861B0F CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 350;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1231 LGSLSNLE 1239
DB 154 LGSLSNLE 162

RESULT 30
ID 095J0 PRELIMINARY; PRT; 360 AA.
AC 095J0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
NCBI_TaxID=9541;
RN [1]
RA SEQUENCE FROM N.A.
RA Tissue-Testis;
RA Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
RT "Isolation of novel full-length cDNA clones from macaque testis cDNA
RT library.",
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AB070191; BAB63136.1;
DR InterPro; IPR000719; Prot kinase.
DR Pfam; PF00069; Kinase; 1_kinase.
KV Hypothetical protein: ATP-binding; transferase.
SQ SEQUENCE 360 AA; 41271 MW; 0697CDA00F34D098 CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 8; Length 360;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1231 LGSLSNLE 1239
DB 164 LGSLSNLE 172

RESULT 31
ID 09LX22 PRELIMINARY; PRT; 414 AA.
AC 09LX22;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
OS Hypothetical 45.6 kDa protein.
GN T31P16_50.
OC Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OX NCBI_TaxID=3702;
RN [1]
RA SEQUENCE FROM N.A.
RA Bevan M., Zimmermann W., Gruenisen A., Warbut R., Kalicki J.,
RA Mohdamin P., Smith A., Bancroft I., Mewes H.W., Rudd S., Lemcke K.,
RA Mayer R.F.X.,
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN (2)
RA SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL, AL356332; CAB92047.1;
DR InterPro; IPR006903; DUF618.
DR InterPro; IPR006569; RPR.
DR Pfam; PF04618; DUF618; 1.
DR SMART; SM00582; RPR; 1.
KV Hypothetical protein.
SQ SEQUENCE 414 AA; 45616 MW; A9C72DEAEC082EC CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 10; Length 414;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 LAKLESEER 42
DB 168 LAKLESEER 176

RESULT 32
ID 09FUP7 PRELIMINARY; PRT; 439 AA.
AC 09FUP7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
OS Genomic DNA, chromosome 5, p1 clone:MON23 (Hypothetical 48.7 kDa
OS protein).
GN MON23.12/ATSG65180.
OC Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Rosidae; 1; Brassicales; Brassicaceae; Arabidopsi.
NCBI_TaxID=3702;
RN [1]
RA SEQUENCE FROM N.A.
RA STRAIN=Columbia;
RA MEDLINE=98403884; PubMed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.,
RL "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RL Sequence features of the regions of 1,367,185 bp covered by 19
RL DNA Res. 5:203-216 (1996).
RN [2]
RA SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
RA Bower L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E.,
RA Lam B., Lin J., Meyer M.C., Miranda M., Nakase M., Nguyen M.,
RA Palm C.J., Sakurai T., Satou M., Seki M., Shim P., Southgate A.,
RA Shiozaki K., Davis R.M., Becker J.R., Theologis A.,
RT "Full length cDNA of gene MON23.12/ATSG65180 (GI:10178180).";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RA SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yu G.,
RA Yamamura Y., Yu G., Yu G., Bower L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyer M.C., Miranda M.,
RA Nakase M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,

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RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.,
 RT "Full Length cDNA of gene MON23.12/AT5G65180 (GI:10178180).",
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB013395; BAB11654.1; -
 DR EMBL; AY034943; AAK59449.1; -
 DR EMBL; AY063122; AL34296.1; -
 DR InterPro; IPR006903; DUF616.
 DR InterPro; IPR006569; RPR.
 DR Pfam; PF04818; DUF618; 1.
 DR SMART; SM00582; RPR; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 439 AA; 48708 MW; 0058A0EFD9CFC31E CRC64;
 Query Match 0.6%; Score 9; DB 10; Length 439;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 34 LAKELBEE 42
 DB 221 LAKELBEE 229
 RESULT 33
 ID 08GUK8 PRELIMINARY; PRT; 469 AA.
 AC 08GUK8;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN ATSG10060.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
 RA Carrincci F., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
 RA Deng J.M., Hayashizaki Y., Heuan V.M., Lee J.W., Ishida J., Kamuya A.,
 RA Kawai J., Kim C.J., Natrasaka M., Onodera C.S., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Shinn P., Tang C.C., Toroumi M., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J., Theologis A.,
 RA Davis R.W.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BT002418; AAC00778.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 469 AA; 51954 MW; B1AB7C0FFFF72FB CRC64;
 Query Match 0.6%; Score 9; DB 10; Length 469;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 34 LAKELBEE 42
 DB 223 LAKELBEE 231
 RESULT 34
 ID 09HY15 PRELIMINARY; PRT; 827 AA.
 AC 09HY15;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Probable transcriptional regulator.
 GN PA3420.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OC NCBI_TaxID=287;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20433337; PubMed=10984043;
 RA Stever C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Collier S.N., Folger K.R., Kas A., Lathig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.B.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 CC -1 SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL
 REGULATORS.
 CC EMBL; AB004763; AAC06808.1; -
 DR InterPro; IPR000792; HTH_LuxR.
 DR Pfam; PF00196; Getz; 1.
 DR PRINTS; PR00038; HTHLUXR.
 DR ProDom; PD000307; HTH_LuxR; 1.
 DR SMART; SM00421; HTH_LuxR; 1.
 DR PROSITE; PS00622; HTH_LuxR_FAMILY; 1.
 KW DNA-binding; Transcription regulation; Complete proteome.
 SQ SEQUENCE 827 AA; 91779 MW; 69BDB9DA552E41FE CRC64;
 Query Match 0.6%; Score 9; DB 16; Length 827;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 472 AGSGKTVLL 480
 DB 42 AGSGKTVLL 50
 RESULT 35
 ID 09ZHM8 PRELIMINARY; PRT; 74 AA.
 AC 09ZHM8;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Pl 15hm2.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OC NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=16M;
 RC MEDLINE=99003167; PubMed=9784561;
 RA Godtfroid F., Tammlau B., Danese I., Dencel P., Tibor A., Weynants V.,
 RA Cloeckert A., Godtfroid J., Letesson J.J.;
 RT "Identification of the peroxamine synthase gene of Brucella
 melitensis 16M and involvement of lipopolysaccharide O side chain in
 RT Brucella survival in mice and in macrophages.";
 RL Infect. Immun. 66:5485-5493(1998).
 DR EMBL; AF047478; AAC98619.1; -
 DR InterPro; IPR002514; Transposase_8.
 DR Pfam; PF01527; Transposase_8; 1.
 SQ SEQUENCE 74 AA; 8301 MW; 872D23DB7F2249D8 CRC64;
 Query Match 0.6%; Score 8; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 59 SEAKRLTK 66
 DB 37 SEAKRLTK 44
 RESULT 36
 ID 09WUH6 PRELIMINARY; PRT; 111 AA.
 AC 09WUH6;

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AC 09MTH6;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE Eapln (Fragment).
GN Eapln (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Testis;
RA Bartles J.R., Zheng L., Li A., Wang M.;
RT "Organization and chromosomal location of the eapln gene in the
RL mouse."
DR Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF14487; A024481.1; -.
DR MGD: MGI:1861630; Eapln.
FT NON_TER 1
FT 111 1
SQ SEQUENCE 111 AA; 13687 MW; 1243020B8580B320 CRC64;

Query Match
Best Local Similarity 0.6%; Score 8; DB 11; Length 111;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 EEBARLAS 165
Db 41 EEBARLAS 46

RESULT 37
006500 PRELIMINARY; PRT; 120 AA.
ID 006500;
AC 006500;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DE V-ATPase proteolipid (Fragment).
OS Desulfurococcus sp. (Strain SY).
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Desulfurococcus.
OC NCBI_TaxId=59822;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=SY;
RA Shibui H., Hamamoto T., Yonda M., Kagawa Y.;
RT "The stabilizing residues and the functional domains in the
RL hyperthermophilic V-ATPase of Desulfurococcus."
DR Biochem. Biophys. Res. Commun. 0:0-0(1997).
DR EMBL: U96487; AAB6412.1; -.
FT NON_TER 1
FT 111 1
SQ SEQUENCE 120 AA; 12638 MW; 0BD47A32A8C25C1A6 CRC64;

Query Match
Best Local Similarity 0.6%; Score 8; DB 1; Length 120;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 ILFGAGLT 110
Db 61 ILFGAGLT 68

RESULT 38
09YDD1 PRELIMINARY; PRT; 146 AA.
ID 09YDD1;
AC 09YDD1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE Hypothetical protein AFB0982.
GN AFB0982.

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OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OC NCBI_TaxId=56636;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=KL;
RA Kawarayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Akai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudo Y.,
RA Yamazaki Y., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
RT "Complete genome sequence of an aerobic hyper-thermophillic
RL crenarchaeon, Aeropyrum pernix KL."
DR DNA Res 6:83-101(1999).
DR EMBL: APO0060; BAA79966.1; -.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 146 AA; 15647 MW; 12F5334D7CB09D47 CRC64;

Query Match
Best Local Similarity 0.6%; Score 8; DB 17; Length 146;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 504 LSLSTRP 511
Db 36 LSLSTRP 43

RESULT 39
09RSR8 PRELIMINARY; PRT; 147 AA.
ID 09RSR8;
AC 09RSR8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein DR2056.
GN DR2056.
OC Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcaceae;
OC Deinococcaceae; Deinococcus.
OC NCBI_TaxId=1299;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Paterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uetrecht T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RL radiodurans R1."
DR Science 286:1571-1577(1999).
DR EMBL: ARO02042; AAF11610.1; -.
DR TIGR: DR2056; -.
DR InterPro: IPR005184; DUF306.
DR Pfam: PF03724; DUF306; 1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 147 AA; 15874 MW; 73CA81D1BDASC78 CRC64;

Query Match
Best Local Similarity 0.6%; Score 8; DB 16; Length 147;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 888 LOGRTTLT 895
Db 109 LOGRTTLT 116

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RESULT 40
 ID Q81R03 PRELIMINARY; PRT; 151 AA.
 AC Q81R03;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE CG4949-PB.
 GN CG4949.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; *Drosophila*.
 NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RL MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Change M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abell J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Baerentzen R.M., Baer A., Baxter J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burlis K.C., Buzam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Houston D., Houtson K.A., Howland T.J., Wei M.H., Idegam C.,
 RA Jaiswal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel P.E., Kodali C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclab J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wesserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zheng F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RL Celniker S.E., Adams M.D., Kornblatter B., Man K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Barton J., An H., Baldwin D., Banison J., Beeson K.Y., Buzam D.A.,
 RA Carlson J.W., Center A., Change M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Drenek D., Fartan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Idegam C., Jaiswal M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson A., Nuno J.,
 RA Paclab J., Patagas A., Park S., Patel S., Pfeiffer B.,
 RA Phuanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svitek R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]

RP SEQUENCE FROM N.A.
 RA Miya S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Bernier B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kornblatter B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Seale S.M.J., Smith A., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RL PLAYBASE;
 DR EMBL; AE003504; AAN09431.1; -;
 SQ SEQUENCE 151 AA; 17120 MW; 8FB66FCBC7026C9A CRC64;
 Query Match 0.6%; Score 8; DB 17; Length 151;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1384 SKYTLTIQ 1391
 DB 13 SKYTLTIQ 20
 RESULT 41
 ID Q30299 PRELIMINARY; PRT; 152 AA.
 AC Q30299;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein AF2371.
 GN AF2371.
 OS Archaeoglobus fulgidus.
 OC Archaeae; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 NCBI_TaxID=2234;
 [1]
 RP SEQUENCE FROM N.A.
 RL STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Kleck H.P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Grim M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kervase A.R., Graham D.E., Kyrides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Peterson S., Retch C.I., McNeil L.K., McKenney K., Adams M.D., Loftus B.,
 RA Kierstead S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.P., McDonald L., Uutterback T.,
 RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 DR EMBL; AB001112; AAB91296.1; -;
 DR TIGR; AF2371; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 152 AA; 16646 MW; E16C36C8124918E CRC64;
 Query Match 0.6%; Score 8; DB 17; Length 152;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1196 VPFVASLP 1203
 DB 95 VPFVASLP 102

RESULT 42

Q9YMI9 PRELIMINARY; PRT; 155 AA.
 ID Q9YMI9
 AC Q9YMI9
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DE Apoptosis inhibitor
 OS Pyruvate kinase
 OC Pyruvate kinase
 NCBI_TaxID=10449;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99124785; PubMed=9887315;
 RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
 RA Slavick J.M., Rohmann G.F.,
 RT "Sequence and analysis of the genome of a baculovirus pathogenic for
 RT Lymantria dispar."
 RL Virology 253:17-34 (1999).
 RP SEQUENCE FROM N.A.
 RA Kuzio J.,
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC EMBL: AF081810; AAC70325.1; .
 DR HSP; Q13490; IOB.
 DR InterPro; IPR001370; BIR.
 DR Pfam; PF00653; BIR; 1.
 DR SMART; SMO0238; BIR; 1.
 DR SMART; SMO0184; RING; 1.
 DR PROSITE; PS01414; BIR_REPEAT_2; 1.
 DR PROSITE; PS00099; ZF_RING_2; 1.
 DR Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 155 AA; 17421 MW; A39B5F0A84740364 CRC64;

Query Match
 Best Local Similarity 0.6%; Score 8; DB 12; Length 155;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 RLASFRNW 169
 DB 7 RLASFRNW 14

RESULT 43

Q8ZU27 PRELIMINARY; PRT; 169 AA.
 ID Q8ZU27
 AC Q8ZU27
 DT 01-MAR-2002 (TEMBLrel. 20, Created)
 DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
 DE Hypothetical protein PAE2531.
 OS Pyrobaculum aerophilum.
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
 NCBI_TaxID=13773;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RA Flitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
 RA Miller J.B.,
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
 RT aerophilum."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
 DR EMBL; AF090882; AL64259.1; .
 InterPro; IPR005593; AAA_Atpase.

DR SMART; SMO0382; AAA; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 169 AA; 18439 MW; FE8233F27669846 CRC64;

Query Match
 Best Local Similarity 0.6%; Score 8; DB 17; Length 169;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 GEAGSGKT 477
 DB 10 GEAGSGKT 17

RESULT 44

Q9Y329 PRELIMINARY; PRT; 192 AA.
 ID Q9Y329
 AC Q9Y329
 DT 01-NOV-1999 (TEMBLrel. 12, Created)
 DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
 DE Putative eapin (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Tissue=Testis;
 RA Tissue=Testis;
 RA Tissue=Testis;
 RA Tissue=Testis;
 RT "Organization and chromosomal location of the eapin gene in the
 RT human."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF134401; AAD24480.1; .
 FT NON TER 1
 FT NON TER 192
 SQ SEQUENCE 192 AA; 21971 MW; 44236A20760AEFE CRC64;

Query Match
 Best Local Similarity 0.6%; Score 8; DB 4; Length 192;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 EEARLAS 165
 DB 116 EEARLAS 123

RESULT 45

Q9VX87 PRELIMINARY; PRT; 197 AA.
 ID Q9VX87
 AC Q9VX87
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DE CG4949 protein (LD46505P).
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Ephydroidea; Ephydroidea; Diptera; Brachycera; Muscomorpha;
 NCBI_TaxID=7227;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX STRAIN=BERKELEY;
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Sutton G.G., Wortman J.R., Richard S.D., Ashburner M., Henderson S.N.,
 RA Britton R.C., Rogers Y.H.C., Blazer R.G., Chang M., Chen L.,
 RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Mikos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-U., Andrews-Pfannkuch C., Baldwin D.,
 RA Bailew R.M., Baeu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolashkov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howard T.J., Wei M.-H., Ibbesman C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milehina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svayras R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Paclob J., Paragas V., Park S., Phuanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003504; AAF48691.1; -
 DR EMBL: AY061506; AAL29054.1; -
 DR FLYBASE: FBgn0030813; CG4549.
 SQ SEQUENCE 197 AA; 22374 MW; 50BFBD40AD775F6 CRC64;
 QY Query Match 0.64; Score 8; DB 5; Length 197;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1384 SKYLILO 1391
 DB 59 SKYLILO 66
 RESULT 46
 ID P91724 PRELIMINARY; PRT; 202 AA.
 AC P91724;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE NULLO (Fragment).
 GN NULLO.
 OS *Drosophila yakuba* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7245;
 RN NCBI_TaxID=7245;
 RP SEQUENCE FROM N.A.
 RC STRAIN=IVORY COAST;
 RX MEDLINE=97051714; PubMed=8896375;
 RA Caccone A., Moriyama E.N., Gleason J.M., Nigro L., Powell J.R.;
 RT "A molecular phylogeny for the *Drosophila melanogaster* subgroup and
 the problem of polymorphism data.";

RL Mol. Biol. Evol. 13:1224-1232(1996).
 DR EMBL: U44732; AAB46423.1; -
 DR FLYBASE: FBgn0020062; Dyak\NULLO.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 202 AA; 22449 MW; F07B623750803D7A CRC64;
 QY Query Match 0.64; Score 8; DB 5; Length 202;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1200 ASLPNPFIS 1207
 DB 23 ASLPNPFIS 30
 RESULT 47
 ID Q8WVNI PRELIMINARY; PRT; 213 AA.
 AC Q8WVNI;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Inhibitor of apoptosis protein-like protein.
 GN IAP.
 OS *Bolletia villosa*.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Pyruidae; Bolletia.
 OX NCBI_TaxID=63515;
 RN NCBI_TaxID=63515;
 RP SEQUENCE FROM N.A.
 RA Davidson B.J., Swalla B.J.;
 RT "A Molecular Analysis of Ascidian Metamorphosis Reveals Activation of
 an Innate Immune Response.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF483030; AAM76110.1; -
 DR InterPro: IPR001370; BIR.
 DR Pfam: PF00653; BIR; 1.
 DR SMART: SM00238; BIR; 1.
 DR PROSITE: PS0143; BIR REPEAT 2; 1.
 SQ SEQUENCE 213 AA; 23948 MW; 4DAJ4B086971007E CRC64;
 QY Query Match 0.64; Score 8; DB 5; Length 213;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 216 EHAKPFX 223
 DB 108 EHAKPFX 115
 RESULT 48
 ID O52735 PRELIMINARY; PRT; 219 AA.
 AC O52735;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE CcMB.
 GN CcMB.
 OS *Rhizobium etli*.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=29449;
 RN NCBI_TaxID=29449;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2;
 RX MEDLINE=97136701; PubMed=8982078;
 RA Aguilar G.R., Soberon M.;
 RT "Cloning and sequence analysis of the *Rhizobium etli* *cma* and *cmb*
 genes involved in c-type cytochrome biogenesis.";
 RL Gene 182:129-135(1996).
 DR EMBL: U52866; AAB40906.1; -

RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brewer V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RT "Full-length cDNA from Arabidopsis thaliana";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY087455; AAC65001.1; -;
 SQ SEQUENCE 232 AA; 26173 MW; ECBE844CF961280D CRC64;

Query Match 0.6%; Score 8; DB 10; Length 232;
 Best Local Similarity 100.0%; Pred. No. 58;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1220 DEBTSEK 1227
 |||||
 DB 145 DEBTSEK 152

RESULT 52

O9LPZ1 PRELIMINARY; PRT; 232 AA.

AC O9LPZ1
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE T23J18.10 (Hypothetical protein).
 GN ATG11430/T23J18.10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosidia I; Brassicales; Brassicaceae; Arabidopsid.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
 RA Kim C., Altafi H., Bei Q., Chin C., Chlou B., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukherjee N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Tortum M., Vaysberg M., Yu G., Federpiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC T23J18 from chromosome
 RT I.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cn. Columbia;
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
 RA Nakajima M., Enju A., Kamaya A., Natsusaka M., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.;
 RT "Arabidopsis thaliana full-length cDNA";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC011661; AAT16628.1; -;
 DR EMBL; AK117508; BAC42171.1; -;
 DR KX Hypothetical protein.
 SQ SEQUENCE 232 AA; 26200 MW; 7E26445D058C24EC CRC64;

Query Match 0.6%; Score 8; DB 10; Length 232;
 Best Local Similarity 100.0%; Pred. No. 58;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1220 DEBTSEK 1227
 |||||
 DB 145 DEBTSEK 152

RESULT 53

O922B4 PRELIMINARY; PRT; 253 AA.

AC O922B4;
 DT 01-MAY-1999 (TRENBLrel. 10, Created)
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE Small espin.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=9437351; PubMed=9763424;
 RA Bartlee J.R., Zheng L., Li A., Wierda A., Chen B.;
 RT "Small espin: A third actin-binding protein and potential forked
 RT protein ortholog in brush border microvilli.";
 RL J. Cell Biol. 143:107-119(1998).
 DR EMBL; AP076856; AAC69563.1; -;
 DR InterPro; IPR003124; WH2; 1.
 DR Pfam; PF02205; WH2; 1.
 DR SMART; SM00246; WH2; 1.
 SQ SEQUENCE 253 AA; 28240 MW; DB40BB6B05F416 CRC64;

Query Match 0.6%; Score 8; DB 11; Length 253;
 Best Local Similarity 100.0%; Pred. No. 63;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 EEBARLAS 165
 |||||
 DB 178 EEBARLAS 185

RESULT 54

O9QY27 PRELIMINARY; PRT; 253 AA.

AC O9QY27
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE Small espin.
 GN ESPN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RX MEDLINE=20056108; PubMed=10588661;
 RA Chen B., Li A., Wang D., Wang M., Zheng L., Bartlee J.R.;
 RT "Espin contains an additional actin-binding site in its N terminus and
 RT is a major actin-binding protein of the Sertoli cell-spermatid
 RT ectoplasmic specialization junctional plaque.";
 RL Mol. Biol. Cell 10:4327-4339(1999).
 DR EMBL; AF14858; AAT18322.1; -;
 DR MGD; MGI:1861630; Espn.
 DR InterPro; IPR003124; WH2.
 DR Pfam; PF02205; WH2; 1.
 DR SMART; SM00246; WH2; 1.
 SQ SEQUENCE 253 AA; 28086 MW; B0247F7128156916 CRC64;

Query Match 0.6%; Score 8; DB 11; Length 253;
 Best Local Similarity 100.0%; Pred. No. 63;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 EEBARLAS 165
 |||||
 DB 178 EEBARLAS 185

RESULT 55

O9DD12 PRELIMINARY; PRT; 253 AA.

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AC Q9D012;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
GN Eapin.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP
RC SEQUENCE FROM N.A.
RA MEDLINE=C57BL/6J; TISSUE=Kidney;
RA Kawai J., Shinagawa A., Shidate K., Yoshino M., Itoh M., Iehi Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi U., Fukuda S.,
RA Aizawa K., Iwasa M., Mihai K., Kiyosawa H., Kondo S., Yamana S.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kabukawa T., Saito R.,
RA Felschmann W., Gaasterland T., Gissi C., King B., Casavant T.,
RA Kuehl P., Lewis S., Mateno Y., Nikaido I., Fesole G., Quackenbush J.,
RA Schirral L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baladevall R., Barsh G.,
RA Brownstein S.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,
RA Chutanchich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauer P.,
RA Saeki H., Sato K., Schoenbach C., Rodriguez I., Sakamoto N.,
RA Suzuki H., Taya-Oka K., Wang K.H., Weitz C., Whitaker J., Wink K.F.,
RA Wyszewski A., Yoshida K., Hasegawa Y., Kawai H., Kohetski S.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001);
DR EMBL; AK002284; BAB21987.1; -
DR MGD; MGI:1861610; Eapin.
DR InterPro; IPR003124; WH2.
DR Pfam; PF02205; WH2; 1.
DR SMART; SM00246; WH2; 1.
SQ SEQUENCE 253 AA; 28097 MW; 97A55A133470F487 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 11; Length 253;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 EEBARLAS 165
Db 178 EEBARLAS 185

RESULT 56
Q9DGN3 PRELIMINARY; PRT; 268 AA.
AC Q9DGN3;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TEMBLrel. 23, Last annotation update)
GN Eapin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP
RC SEQUENCE FROM N.A.
RA TISSUE=Cochlea;
RA MEDLINE=20427267; PubMed=10975527;
RA Zheng L., Sekerkova G., Vranich K., Tilly L.G., Mugnaini E.,
RA Bartles J.R.;
RT "The Deaf Jerker Mouse Has a Mutation in the Gene Encoding the Eapin
Cell 102:377-384(2000).
EMBL; AF239855; AAF98133.1; -

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DR InterPro; IPR000381; Inhibin betaB.
DR InterPro; IPR002865; P-rich_exten.
DR InterPro; IPR006077; Vinculin/catenin.
DR Pfam; PR02025; WH2.
DR PRINTS; PRO0671; INHIBINB.
DR PRINTS; PRO1217; PRICHEXTEN.
DR SMART; SM00806; VINCULIN.
DR SMART; SM00246; WH2; 1.
FT NON TER 1
SQ SEQUENCE 268 AA; 29103 MW; F81584828B2B9A2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 13; Length 268;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 EEBARLAS 165
Db 192 EEBARLAS 199

RESULT 57
Q9PLC0 PRELIMINARY; PRT; 307 AA.
AC Q9PLC0;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE Transcriptional activator protein mdk.
GN NHR OR C0025.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=217992;
RN [1]
RP
RC SEQUENCE FROM N.A.
RA STRAIN=06:HI / CFT073 / ATCC 700928;
RA MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G., III, Redford P., Roesch P.,
RA Rayko D., Buckles E.L., Iliou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016755; AAN78525.1; -
SQ SEQUENCE 307 AA; 34965 MW; 557B80FF7BC141F CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 16; Length 307;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1275 NDSVVEI 1282
Db 259 NDSVVEI 266

RESULT 58
Q9X6W1 PRELIMINARY; PRT; 314 AA.
AC Q9X6W1;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DE Class A beta-lactamase precursor TLA-1 (EC 3.5.2.6).
GN TLA-1.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=562;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=20187162; PubMed=10722503;
RA Silva J., Aguilar C., Ayala G., Bettrada M.A., Garza-Ramos U.,
RA Lara-Lemus R., Ledezma L.;
RT "TLA-1: a new plasmid-mediated extended-spectrum beta-lactamase from
RT *Escherichia coli*."
RL Antimicrob. Agents Chemother. 44:997-1003 (2000).
DR EMBL: AF148067; AAD37403.1; -.
DR HSSP: P00807; 1BLP.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; Beta_lactamase_1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolyase; Plasmid.
SQ SEQUENCE 314 AA; 34980 MW; 1FEB53E011D7A53 CRC64;

Query Match 0.6%; Score 8; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 683 ELKATVS 690
Db 136 ELKATVS 143
|||||
Q98JF7 PRELIMINARY; PRT; 315 AA.
ID Q98JF7
AC Q98JF7
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein ml11963.
GN ML11963.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Mesorhizobium.
OC NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAF303039;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Kishida Y., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT *Mesorhizobium loti*."
RL DNA Res. 7:331-338 (2000).
DR EMBL: AP002998; BAB9209.1; -.
DR InterPro: IPR001279; Blactamase-like.
DR Pfam: PF00753; lactamase_B; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 315 AA; 34032 MW; 7D28710A057035F7 CRC64;

Query Match 0.6%; Score 8; DB 16; Length 315;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 297 AALAKGL 304
Db 72 AALAKGL 79
|||||
Q46012 PRELIMINARY; PRT; 329 AA.
ID Q46012
AC Q46012
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE ZK228.7 protein.
GN ZK228.7.
OS Caenorhabditis elegans.
OC Euarystota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Bushman V.M.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
RN (2)
RP MEDLINE=99069613; PubMed=9851916;
RP SEQUENCE FROM N.A.
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018 (1998).
DR EMBL: ZK228.7; CAB04998.1; -.
DR WormPep; ZK228.7; CE16716.
DR InterPro: IPR003003; 7TM_chemo2.
DR InterPro: IPR00168; 7TM_nematode.
DR Pfam: PF01604; 7tm_5; 1.
SQ SEQUENCE 329 AA; 36804 MW; F785BACA2AFB24C CRC64;

Query Match 0.6%; Score 8; DB 5; Length 329;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1072 LLTLTSL 1079
Db 249 LLTLTSL 256
|||||
Q8XVS1 PRELIMINARY; PRT; 331 AA.
ID Q8XVS1
AC Q8XVS1
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Probable L-arabinose-binding periplasmic (PBP) ABC transporter
DE protein.
GN ARAV OR RSC2758 OR RS00096.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX -MEDLINE=21681879; PubMed=11823852;
RA Saratombat M., Genin S., Artiguenave F., Gouzy J., Mengnot S.,
RA Alet M., Billault A., Brotier P., Camue J.C., Catolico L.,
RA Chander M., Choisme N., Claudel-Renard C., Cunne S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Signier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum."
RL Nature 415:457-502 (2002).
DR EMBL: AL646071; CAD16465.1; -.
DR InterPro: IPR001761; Periplasm/Pac1.
DR Pfam: PF00532; Peripla_BP_1like; 1.
KW Complete proteome.
SQ SEQUENCE 331 AA; 35427 MW; 5BFB4064C0F16F8P CRC64;

Query Match 0.6%; Score 8; DB 16; Length 331;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 296 VALAKAG 303
Db 184 VALAKAG 191
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RESULT 62
ID 093B95 PRELIMINARY; PRT; 343 AA.
AC 093B95;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DE D-1-OCT-2002 (TRENBLREL. 22, Last annotation update)
GN D-alanine:D-alanine ligase 2.
OS Enterococcus gallinarum.
OC Bacteria; Firmicutes; Lactobactiales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1353;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BM4174;
RA Ambur O.H.; Reynolds P.E.; Arias C.A.;
RT "Characterization of a D-Ala:D-Ala ligase gene flanking the vanc
RT resistant evidence for the presence of three ligase genes in vancomycin
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL:AB93615; AAK97387.1; -.
DR InterPro:IPR000291; Data_1lgVan.
DR Pfam:PF01820; Data_1lgVan.
KW ligase.
SQ SEQUENCE 343 AA; 38454 MW; 4B0E928BF15742F CRC64;
Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 343;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 423 DISIDLAT 430
DB 260 DISIDLAT 267

RESULT 63
ID 057896 PRELIMINARY; PRT; 345 AA.
AC 057896;
DT 01-AUG-1998 (TRENBLREL. 07, Created)
DT 01-AUG-1998 (TRENBLREL. 07, Last sequence update)
DE 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE 345AA long hypothetical transport-ATP binding protein.
GN PH0157.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae; Thermococcaceae.
NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=OT3;
RA MEDLINE=9814137; PubMed=9679194;
RA Kawarabayashi Y.; Sawada M.; Horikawa H.; Hatakeyama Y.; Hino Y.;
RA Yamamoto S.; Sekine M.; Baba S.-I.; Koseki H.; Hoshino A.; Nagai Y.;
RA Sakai M.; Gura K.; Otsuka R.; Nakazawa H.; Takamiya M.; Ohfuku Y.;
RA Furukawa T.; Tanaka T.; Kudo Y.; Yamazaki O.; Kishida N.; Gouchi A.;
RA Maechi Y.; Shizuya H.; Nakamura Y.; Kobb F.T.; Horikoshi K.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS).
DR EMBL:AB000001; BAA9226.1; -.
DR HSP; Q58663; 166H.
DR InterPro:IPR003593; AAA_ATPase.
DR InterPro:IPR004139; ABC_transporter.
DR InterPro:IPR005116; TOBE.
DR Pfam:PF00005; ABC_tran; 1.
DR Pfam:PF03459; TOBE; 1.
DR ProDom:PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.

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DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport; Complete proteome.
SQ SEQUENCE 345 AA; 38927 MW; 98B76ADB8F74C1EF CRC64;
Query Match
Best Local Similarity 100.0%; Score 8; DB 17; Length 345;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 473 GSGKTVLL 480
DB 36 GSGKTVLL 43

RESULT 64
ID 08LB55 PRELIMINARY; PRT; 358 AA.
AC 08LB55;
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DE 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Putative aldolase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsia.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J.; Volfovsky N.; Town C.D.; Torkhan M.; Alexandrov N.;
RA Feldmann K.A.; Flavell R.B.; White O.; Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brewer V.; Torkhan M.; Alexandrov N.; Lu Y.-P.; Flavell R.;
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL:AY087414; AAM64563.1; -.
SQ SEQUENCE 358 AA; 38345 MW; 4B30B2AF060D421B CRC64;
Query Match
Best Local Similarity 100.0%; Score 8; DB 10; Length 358;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 145 LKSLRRCG 152
DB 80 LKSLRRCG 87

RESULT 65
ID 082487 PRELIMINARY; PRT; 358 AA.
AC 082487;
DT 01-NOV-1998 (TRENBLREL. 08, Created)
DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
DE 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE T12H20.10 protein (putative aldolase)
GN T12H20.10 OR AT4G10750 OR AT4G10750/T12H20.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsia.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RA WASHU;
RT "The A. thaliana Genome Sequencing Project."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

```

RC STRAIN=cv. Columbia;
 RA Cotton M., Graves T., Suterer C., Modde T.;
 RT "The sequence of A. thaliana T12H20."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Waterston R.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF080119; AAC35519.1; -;
 DR EMBL; AL161518; CAB81176.1; -;
 DR EMBL; AK118216; BAC42838.1; -;
 DR HSSP; P23522; 1DXE.
 DR InterPro; IPR005000; HpcH Hpal.
 DR Pfam; PF03328; HpcH Hpal; 1.
 SQ SEQUENCE 358 AA; 38404 MW; E932B2AF060ECFAD CRC64;

Query Match 0.6%; Score 8; DB 10; Length 358;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 LKSLRRCG 152
 DB 80 LKSLRRCG 87

RESULT 66
 ID Q97H79 PRELIMINARY; PRT; 365 AA.
 AC Q97H79;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Predicted GTPase, YTAI B. subtilis ortholog.
 GN CAC2134.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 NCBI_TaxID=1488;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; Pubmed=1146286;
 RA Noelling J., Biston G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabachev F., Doucet-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF080119; AAC35519.1; -;
 DR EMBL; AL161518; CAB81176.1; -;
 DR EMBL; AK118216; BAC42838.1; -;
 DR HSSP; P23522; 1DXE.
 DR InterPro; IPR005000; HpcH Hpal.
 DR Pfam; PF03328; HpcH Hpal; 1.
 SQ SEQUENCE 358 AA; 38404 MW; E932B2AF060ECFAD CRC64;

DR TIGRPFAM; TIGR00092; TIGR00092; 1.
 KW Complete proteome.
 SQ SEQUENCE 365 AA; 40607 MW; 13CD1F39C2B8D2AD CRC64;

Query Match 0.6%; Score 8; DB 16; Length 365;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 LEEEOKE 45
 DB 249 LEEEOKE 256

RESULT 67
 ID Q92NG8 PRELIMINARY; PRT; 372 AA.
 AC Q92NG8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative ABC transporter ATP-binding protein.
 GN R02237 OR SMC01625.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium.
 NCBI_TaxID=382;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396507; Pubmed=11481430;
 RA Capela D., Barloy-Hubier F., Gouzy J., Bothe G., Ampe F., Batur J.,
 RA Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godie T., Goffeau A., Kahn D., Kiss B., Lelaure V., Maury D.,
 RA Pohl T., Portetelle D., Puhler A., Purnelle B., Rampelberg U.,
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 Sinorhizobium meliloti strain 1021."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 DR EMBL; AL591790; CAC46816.1; -;
 DR InterPro; IPR003593; AAA ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00005; ABC_tran; 1.
 DR SMART; SM00382; AAA; 1.
 KW Complete proteome.
 SQ SEQUENCE 372 AA; 39835 MW; 6DF9BF0C39C3502C CRC64;

Query Match 0.6%; Score 8; DB 16; Length 372;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 GSGKTVLL 480
 DB 39 GSGKTVLL 46

RESULT 68
 ID Q8DT00 PRELIMINARY; PRT; 372 AA.
 AC Q8DT00;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Conserved hypothetical protein.
 GN SMU1280C.
 OS Streptococcus mutans.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 NCBI_TaxID=1309;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UA159 / ATCC 700610 / Serotype C;
 RX MEDLINE=22295063; Pubmed=12397186;
 RA Ajdic D., Mchman W.M., McLaughlin R.E., Savic G., Chang J.,

RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
 RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Perrett J.J.,
 RT Genome sequence of *Streptococcus mutans* UA159, a cariogenic dental
 RL pathogen.
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
 DR EMBL, AF014963; AAS58960.1; -
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 372 AA; 42793 MW; 76D427DB50B51ED CRC64;

Query Match

Best Local Similarity 0.6%; Score 8; DB 16; Length 372;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1235 SNEEIL 1242
 DB 137 SNEEIL 144

RESULT 69

ID 098DC3 PRELIMINARY; PRT; 390 AA.
 AC 098DC3;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DE N-acetylglucosamine-6-phosphate deacetylase.
 GN MLL4766.
 OS Rhizobium loci (Mesorhizobium loci).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 RN NCBI_Taxid=381;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Marahaba A., Ideeswa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimizu S., Sugimoto M.,
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loci."
 RL DNA Res. 7:331-338(2000).
 DR EMBL, AP003004; BAB51348.1; -
 DR InterPro; IPR006680; Amdohydro_1.
 DR InterPro; IPR003764; Naga.
 DR Pfam; PF01979; Amdohydro_1; 1.
 DR PRODOM; PD001248; Naga; 1.
 DR TIGRFAMs; TIGR00221; naga; 1.
 KW Complete proteome.
 SO SEQUENCE 390 AA; 40090 MW; AC312A1F1A9F688 CRC64;

Query Match

Best Local Similarity 0.6%; Score 8; DB 16; Length 390;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 VVALARAG 303
 DB 183 VVALARAG 190

RESULT 70

ID 054143 PRELIMINARY; PRT; 391 AA.
 AC 054143;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DE Acyl-CoA dehydrogenase Redw.
 GN Redw OR SC05879 OR SC269.20.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteridae; Actinomycetales;
 OC Streptomyces; Streptomycetaceae; Streptomyces.

OX NCBI_Taxid=1902;
 RN [1] -

RC SEQUENCE FROM N.A.
 RC STRAIN=A3(2);

RA Oliver K., Harris D.,
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);
 RA Parhill J., Barrett B.G., Rajandream M.A.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);

RA Redenbach M., Klesner H.M., Denapate D., Elchner A., Cullum J.,
 RL Kinashi H., Hopwood D.A.;

RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;

RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thompson N.R., James K.D., Harris D.R., Quail M.A., Klesner H.,
 RA Harper D., Bateman A., Brown S., Chandra C., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Klesner T., Lake J., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrett B.G., Parkhill J.,
 RT Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2)";
 RL Nature 417:41-4147(2002).
 DR EMBL, AL339125; CA61468.1; -

DR HSSP; 006319; 1BNC.
 DR InterPro; IPR006090; Acyl-CoA dh_C.

DR InterPro; IPR006091; Acyl-CoA dh_C.
 DR InterPro; IPR006092; Acyl-CoA dh_M.

DR Pfam; PF00441; Acyl-CoA dh; 1_N.
 DR Pfam; PF02770; Acyl-CoA dh; 1_N.

DR Pfam; PF02771; Acyl-CoA dh_M; 1.
 KW Complete proteome.
 SO SEQUENCE 391 AA; 41624 MW; 95E01740EC1EB755 CRC64;

Query Match

Best Local Similarity 0.6%; Score 8; DB 16; Length 391;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LGSDAVOL 34
 DB 334 LGSDAVOL 341

RESULT 71

ID 004151 PRELIMINARY; PRT; 396 AA.
 AC 004151;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE RhoP1 protein precursor.
 GN RhoP1.
 OS Toxoplasma gondii.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriidae; Sarcocystidae;
 OC Toxoplasma.
 OC NCBI_Taxid=5811;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RH;
 RX MEDLINE=92178277; PubMed=1542304;

RA Oseorio P.N., Schwartzman J.D., Boothroyd J.C.;
 RT "A Toxoplasma gondii thoptry protein associated with host cell
 penetration has unusual charge asymmetry.";
 RL Mol. Biochem. Parasitol. 50:1-15(1992).
 DR EMBL; M71274; AAA69859.1; -
 DR InterPro; IPR002965; P-rich extensn.
 DR PRINTS; PR01217; PRICHEXTENSN.
 KW Signal.
 FT SIGNAL. 1 21
 FT CHAIN 22 396 RHOPTRY PROTEIN.
 SQ SEQUENCE 396 AA; 42670 MW; 929A1B12540E99E7 CRC64;
 QY Query Match 0.6%; Score 8; DB 5; Length 396;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 105 FGAGLRRL 112
 363 FGAGLRRL 370
 RESULT 72
 ID 08JHV9 PRELIMINARY; PRT; 401 AA.
 AC 08JHV9.
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE IAP-like protein.
 GN XlX.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22038366; PubMed=12021770;
 RA Holley C.L., Olson M.R., Colon-Ramos D.A., Kornbluth S.;
 RT "Reaper eliminates IAP proteins through stimulated IAP degradation and
 RT generalized translational inhibition.";
 RL Nat. Cell Biol. 4:439-444(2002).
 DR EMBL; AF468029; AAM88215.1; -
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00653; BIR; 2.
 DR SMART; SMO0238; BIR; 2.
 DR PROSITE; PS01282; BIR_REPEAT_1; 2.
 DR PROSITE; PS0145; BIR_REPEAT_2; 2.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 401 AA; 45286 MW; F8FDD31AFBFD146 CRC64;
 QY Query Match 0.6%; Score 8; DB 13; Length 401;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 195 VQCFSCGG 202
 76 VQCFSCGG 83
 RESULT 73
 ID 09V106 PRELIMINARY; PRT; 422 AA.
 AC 09V106.
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Hypothetical protein PAB0247.
 GN PAB0247.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;

OC Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GES / Oresay;
 RA Heilig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 RT structure and evolution";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ248284; CAB49293.1; -
 DR InterPro; IPR004365; tRNA_anti.
 DR Pfam; PF01336; tRNA_anti; 1.
 SQ SEQUENCE 422 AA; 48560 MW; 518B6DA0EB10D978 CRC64;
 QY Query Match 0.6%; Score 8; DB 17; Length 422;
 Best Local Similarity 100.0%; Pred. No. 98;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1353 LPRDLRLN 1360
 38 LPRDLRLN 45
 RESULT 74
 ID 098CE6 PRELIMINARY; PRT; 429 AA.
 AC 098CE6.
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE Nicotinamide nucleotide transhydrogenase, subunit alpha.
 GN MRS181.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=1124968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idehara K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003005; BAB51675.1; -
 DR InterPro; IPR004002; Aladh_PRT.
 DR Pfam; PF01262; Aladh_PRT; 1.
 KW Complete proteome.
 SQ SEQUENCE 429 AA; 44262 MW; 805F2C6ACF393406 CRC64;
 QY Query Match 0.6%; Score 8; DB 16; Length 429;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 296 VVALAKAG 303
 104 VVALAKAG 111
 RESULT 75
 ID 098C91 PRELIMINARY; PRT; 437 AA.
 AC 098C91.
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Exopolysaccharide production protein, ExoQ.
 GN MRS243.

OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 RX NCBI_TaxID=381;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFP303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti."
 RL DNA Rep. 7:331-338(2000).
 DR EMBL: AP003006; BAB51730.1;
 DR Fiterpro: IPR007016; Wzy_C;
 DR Pfam: PF04932; Wzy_C; 1.
 KW Complete proteome.
 SQ SEQUENCE 437 AA; 48542 MW; 33BBBACD861CFC3C CRC64;
 Query Match 0.64; Score 8; DB 16; Length 437;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 891 RTLTGAL 898
 |||||
 Db 112 RTLTGAL 119

Search completed: December 18, 2003, 09:15:01
 Job time : 84 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 09:11:49 : Search time 22 Seconds
(without alignments)
2999.021 Million cell updates/sec

Title: US-09-830-338-1

Perfect score: 1403

Sequence: 1 MATOQKASDERISQFDHNL.....SKYTLIQWLPSPILQK 1403

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1403	100.0	1403	1	BIR1_HUMAN
2	35	2.5	1447	1	BIR6_MOUSE
3	24	1.7	1402	1	BIR6_MOUSE
4	24	1.7	1403	1	BIR6_MOUSE
5	24	1.7	1403	1	BIR6_MOUSE
6	24	1.7	1403	1	BIR6_MOUSE
7	8	0.6	156	1	MUSB_MYCTU
8	8	0.6	179	1	OP1A_HUMAN
9	8	0.6	272	1	DNRI_STRPE
10	8	0.6	290	1	YAS7_METUA
11	8	0.6	324	1	FABH_RHOCA
12	8	0.6	335	1	SPPA_BACSU
13	8	0.6	382	1	KCC1_METAN
14	8	0.6	421	1	SAHI_PYRFO
15	8	0.6	421	1	SAHI_PYRFO
16	8	0.6	489	1	GSPA_ECOLI
17	8	0.6	496	1	BIR4_MOUSE
18	8	0.6	496	1	BIR4_MOUSE
19	8	0.6	548	1	AMDS_EMENTI
20	8	0.6	1338	1	ACIN_MOUSE
21	8	0.6	1341	1	ACIN_HUMAN
22	8	0.6	1449	1	DPO3_CLOPE
23	8	0.5	90	1	VAS4_VACCV
24	7	0.5	98	1	YS15_BOBBU
25	7	0.5	106	1	V266_RICPR
26	7	0.5	117	1	TLB2_MOUSE
27	7	0.5	121	1	YFL4_ARATH
28	7	0.5	134	1	YHCB_ECOLI
29	7	0.5	155	1	IL2_CAPHI
30	7	0.5	175	1	YB43_MYCPN
31	7	0.5	178	1	DSBB_PASMU
32	7	0.5	181	1	HP28_HUMAN
33	7	0.5	184	1	MPL_MPLV

34	7	0.5	196	1	T2D9_DROME
35	7	0.5	207	1	PSM9_PYRAB
36	7	0.5	224	1	DCL_LYCES
37	7	0.5	230	1	DAG_ANTWA
38	7	0.5	231	1	ARAD_BACHD
39	7	0.5	232	1	SMY_MOUSE
40	7	0.5	232	1	SPH_HUMAN
41	7	0.5	237	1	SPIN_HUMAN
42	7	0.5	239	1	CALD_METCA
43	7	0.5	240	1	SPIN_MOUSE
44	7	0.5	258	1	COD1_CLOPE
45	7	0.5	258	1	SPN2_HUMAN
46	7	0.5	259	1	MOB2_YEAST
47	7	0.5	260	1	CCG6_HUMAN
48	7	0.5	260	1	CCG6_MOUSE
49	7	0.5	260	1	CCG6_RAT
50	7	0.5	261	1	COD1_STRMU
51	7	0.5	269	1	AROB_NATMU
52	7	0.5	281	1	YQAC_LACLA
53	7	0.5	284	1	MRP_CLOPE
54	7	0.5	286	1	IAP1_NPVAC
55	7	0.5	289	1	ZNF75_HUMAN
56	7	0.5	292	1	METP_BUCAP
57	7	0.5	295	1	RRSC_MYXXA
58	7	0.5	295	1	Y326_MYXGE
59	7	0.5	296	1	NIPD_NOSCO
60	7	0.5	298	1	BIR7_HUMAN
61	7	0.5	300	1	GLXB_RHIME
62	7	0.5	304	1	HEMK_MYCTU
63	7	0.5	308	1	BEL1_SFVI
64	7	0.5	308	1	CITR_BACSU
65	7	0.5	315	1	GLS4_RHIME
66	7	0.5	323	1	RRC4_YEAST
67	7	0.5	329	1	DAPF_LISMO
68	7	0.5	330	1	KDHA_BACSU
69	7	0.5	337	1	YB21_YEAST
70	7	0.5	337	1	YQ42_CLOPE
71	7	0.5	350	1	TGDS_HUMAN
72	7	0.5	350	1	UXUX_CLOPE
73	7	0.5	352	1	HIS6_STRAW
74	7	0.5	352	1	HIS6_STRAW
75	7	0.5	352	1	HIS6_STRAW
76	7	0.5	355	1	TGDS_MOUSE
77	7	0.5	355	1	Y124_AOUAE
78	7	0.5	363	1	PIAP_PIG
79	7	0.5	363	1	DP3B_AOUAE
80	7	0.5	363	1	MODC_RHOCA
81	7	0.5	363	1	MURC_LISIN
82	7	0.5	363	1	YK12_CABEL
83	7	0.5	364	1	AKRA_DROME
84	7	0.5	366	1	VP09_BRAPS
85	7	0.5	372	1	TAL2_STRCO
86	7	0.5	375	1	GLK1_TRIVA
87	7	0.5	376	1	MPK2_ARATH
88	7	0.5	378	1	FEN1_MOUSE
89	7	0.5	378	1	YNN1_ANASP
90	7	0.5	380	1	THIT_THETN
91	7	0.5	404	1	THIT_THETN
92	7	0.5	408	1	PGK_THEAC
93	7	0.5	411	1	FKB3_YEAST
94	7	0.5	416	1	PROA_VIBVU
95	7	0.5	417	1	YAT1_SYNP6
96	7	0.5	423	1	CESS_HUMAN
97	7	0.5	427	1	SYS_CHLTE
98	7	0.5	428	1	PURA_STRPN
99	7	0.5	430	1	SURA_BUCAL
100	7	0.5	432	1	MURD_FUSNN

ALIGNMENTS

P49906	Drosophila
Q94090	Pyrococcus
Q42463	Lycopodium
Q38732	Antirrhinum
Q98494	Bacillus ha
P13675	Mus musculus
Q99865	Mus musculus
O96567	Mus musculus
P13505	Meleagris g
Q61142	Mus musculus
Q8XJ22	Clostridium
Q9P222	Mus musculus
P43563	Saccharomyces
O9PXC2	Mus musculus
O8YHW7	Mus musculus
P53388	Streptococcus
P53389	Streptococcus
Q9C1B9	Leptococcus
P53381	Clostridium
P41435	Autographa
P51815	Mus musculus
O8KA62	Buchnera ap
O07083	Myxococcus
P47568	Myxococcus
P52337	Nostoc comm
Q96635	Mus musculus
O87390	Rhizobium m
O10602	Myxococcus
P23169	Asiatic foam
P31917	Bacillus su
O92P80	Rhizobium m
P40339	Saccharomyces
Q8Y5N9	Listeria mo
O32147	Bacillus su
P38278	Saccharomyces
Q8XHP0	Clostridium
O95455	Mus musculus
O8XP15	Clostridium
O93VP9	Staphylococcus
O8XN33	Staphylococcus
O8YD17	Mus musculus
O67685	Aquifex aeo
O62640	Sus scrofa
O67725	Aquifex aeo
O08381	Rhodospirillum
O929Y2	Listeria in
O8Y5M2	Listeria in
P42169	Cenozoanthus
P13172	Drosophila
O9C119	Bacteriophage
O9XAC0	Streptococcus
O9GTC9	Trichomonas
O33022	Arabidopsis
P19742	Mus musculus
P40080	Anabaena sp
O8Y910	Thermoplasma
Q91804	Bacillus ha
O91891	Saccharomyces
O8E194	Vibrio vuln
P08444	Streptococcus
O9XW77	Mus musculus
O8RE66	Chlorobium
O9T1C1	Streptococcus
P57240	Buchnera ap
O8YDQ1	Leptococcus

RESULT 1

BIR1_HUMAN
 ID BIR1_HUMAN STANDARD, PRT, 1403 AA.
 AC Q13075, Q75857, Q13730, Q99796;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-1997 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 1 (neuronal apoptosis
 DE inhibitor protein).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid:9606;
 RN 1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RA Roy N., Mahadevan M.S., McLean M., Shuter G., Yaraqi Z.,
 RA Farahani R., Baird S., Besner-Johnson A., Lefebvre C., Kang X.,
 RA Saito H., Aubry H., Tamai K., Guan X., Iomann P., Crawford T.O.,
 RA de Jong P.J., Suth L., Ikeda J., Korneluk R.G., Mackenzie A.,
 RT "The gene for neuronal apoptosis inhibitor protein is partially
 RT Cell 80:167-178(1995).
 RN 12)
 RP SEQUENCE FROM N.A., AND REVISIONS.
 RC TISSUE=Brain;
 RA Chen Q., Baird S.D., Mahadevan M., Besner-Johnson A., Farahani R.,
 RA Xuan J.-Y., Kang X., Lefebvre C., Ikeda J.-E., Korneluk R.G.,
 RA Mackenzie A.E.;
 RT "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular
 RT atrophy candidate genes SMN and NAIP.";
 RN 13)
 RP SEQUENCE OF 386-623 FROM N.A.
 RA der Steege G., Draefler T.G., Grotschohlen P.M., Otinga J.,
 RA Anzeino R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,
 RA Buys C.H.C.M.;
 RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN 14)
 RP SEQUENCE OF 222-1403 FROM N.A.
 RA Jones K., Graves T., McPherson J.;
 RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN 15)
 RP FUNCTION.
 RC TISSUE=Liver;
 RA MEDLINE=96149249; PubMed=8552191;
 RA Liebon P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
 RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.,
 RT Suppression of apoptosis in mammalian cells by NAIP and a related
 RT family of IAP genes.";
 RN Nature 379:349-353(1996).
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
 CC SIGNALS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY
 CC NEURONS. FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN
 CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN
 CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE I). SMAS
 CC ARE PARTIAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE I
 CC (WERNIG-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE
 CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE
 CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO
 CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000
 CC MEMBERS.
 CC -1- SIMILARITY: Contains 3 BIR repeats.
 CC -1- SIMILARITY: Contains 1 NACHT domain.
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 DR EMBL: U19251; AAC52045.1; -
 DR EMBL: U80017; AAC52047.1; -
 DR EMBL: U21913; AAA64504.1; -
 DR EMBL: AC005031; AAC62261.1; -
 DR HSSP: Q13490; IOBH.
 DR Genew: HGNC:7634; BIR1.
 DR MIM: 600355; -
 DR GO: GO:0008189; F:apoptosis inhibitor activity; TAS.
 DR GO: GO:0006916; P:anti-apoptosis; TAS.
 DR GO: GO:0007399; P:neurogenesis; TAS.
 DR Interpro: IPR003593; AAA_NTPase.
 DR Interpro: IPR001370; BIR.
 DR Pfam: PF00553; BIR; 3.
 DR SMART: SM00382; AAA; 1.
 DR SMART: SM00238; BIR; 3.
 DR PROSITE: PS01282; BIR_REPEAT_1; 3.
 DR PROSITE: PS01443; BIR_REPEAT_2; 3.
 DR PROSITE: PS00837; NACHT; 1.
 KW Apoptosis; Repeat.
 FT REPEAT 60 127 BIR 1.
 FT REPEAT 159 227 BIR 2.
 FT REPEAT 278 345 BIR 3.
 FT DOMAIN 464 758 NACHT.
 FT CONFLICT 222 223 PK -> YR (IN REF. 4).
 FT CONFLICT 386 387 VP -> ST (IN REF. 3).
 FT CONFLICT 535 535 M -> V (IN REF. 3).
 FT CONFLICT 553 553 Y -> H (IN REF. 3).
 FT CONFLICT 1221 1221 MISSING (IN REF. 4).
 SQ SEQUENCE 1403 AA; 159613 MW; 566304C15D4A5B64 CRC64;
 Query Match 100.0%; Score 1403; DB 1; Length 1403;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATOQKASDERISQFPHNLPELSALIGDAVOLANLEBEBOKERAKQGVNSQMRSE 60
 DB 1 MATOQKASDERISQFPHNLPELSALIGDAVOLANLEBEBOKERAKQGVNSQMRSE 60
 QY 61 AKRLKTPVTEPYSSWIPQEMAAAGFTFTVNSGIQCFCSLIFGAGLTRLEIDHKRF 120
 DB 61 AKRLKTPVTEPYSSWIPQEMAAAGFTFTVNSGIQCFCSLIFGAGLTRLEIDHKRF 120
 QY 121 HPDCGFLNKDVGNIATKVDIVRNKLSRLGCKAKRYQEBEARKLASPNNPFTYQGISFCV 180
 DB 121 HPDCGFLNKDVGNIATKVDIVRNKLSRLGCKAKRYQEBEARKLASPNNPFTYQGISFCV 180
 QY 181 LSEAGVFETGQDVTQVCFSCGCGCLGNWSEGDPPMKHAKKPYVCEFLARKSSSEITQYI 240
 DB 181 LSEAGVFETGQDVTQVCFSCGCGCLGNWSEGDPPMKHAKKPYVCEFLARKSSSEITQYI 240
 QY 241 OSYKGFVDITGEHFNVSQVRELPMASAYCNDISFAVEELRLDSFKDPPRESAVGVAALA 300
 DB 241 OSYKGFVDITGEHFNVSQVRELPMASAYCNDISFAVEELRLDSFKDPPRESAVGVAALA 300
 QY 301 KAGLFTYGIKDIQVCFSCGCGCLGNWSEGDPPMKHAKKPYVCEFLARKSSSEITQYI 360
 DB 301 KAGLFTYGIKDIQVCFSCGCGCLGNWSEGDPPMKHAKKPYVCEFLARKSSSEITQYI 360
 QY 361 RGEICELLETTSESLSRSTIAVGIVYVEMAOGBAQMFOEAKNLAEQILRAVYTSASFRMS 420
 DB 361 RGEICELLETTSESLSRSTIAVGIVYVEMAOGBAQMFOEAKNLAEQILRAVYTSASFRMS 420
 QY 421 LLDISSDLATHLGCGCLSTASGHSKPVQEPVLYPEVFGNLNWSVCVGGESGKTYLL 480
 DB 421 LLDISSDLATHLGCGCLSTASGHSKPVQEPVLYPEVFGNLNWSVCVGGESGKTYLL 480
 QY 481 KTIAPLWASGCCPLNRPQIVFYLSLSTRPDEGLASIIICDQLERKSGSVTEMCMRNIIQ 540


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Db 481 KKIAPLWASGCGPLNPFQVPLSLSTRPDBGLASTICDDELEKESVEMCKRNIIQ 540
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Db 541 QKNOVFLDDYKEICISIPQVIGKLIQKNHLSRTCLIAVATNRADIRREYLEIIEIK 600
Oy 601 AAPPNVNVCILRKLFSSNMTRAKRPFWYRGKQKSLQKQKTELPFAALCAMFQYPPDS 660
Db 601 AAPPNVNVCILRKLFSSNMTRAKRPFWYRGKQKSLQKQKTELPFAALCAMFQYPPDS 660
Oy 661 FDDVAVFESYMERLSLNKKAETAILKATVSSCGEIALKGFSCCFEPNDLAEAGVED 720
Db 661 FDDVAVFESYMERLSLNKKAETAILKATVSSCGEIALKGFSCCFEPNDLAEAGVED 720
Oy 721 EDLMCMKSKTAORLAPFRPLSPAFOEFLAGMRLIELLDDRDREHDDLGLYHKOINS 780
Db 721 EDLMCMKSKTAORLAPFRPLSPAFOEFLAGMRLIELLDDRDREHDDLGLYHKOINS 780
Oy 781 PMMTVSANNFLNVSLSPTKAGPKIVSHLLVLVDNKESELENISENDYLLKQPEISLQ 840
Db 781 PMMTVSANNFLNVSLSPTKAGPKIVSHLLVLVDNKESELENISENDYLLKQPEISLQ 840
Oy 841 MOLRGWMOICPOYFEMSEHLLVLAATAVQSNVAAQSPFVLOFQGRITLGLNL 900
Db 841 MOLRGWMOICPOYFEMSEHLLVLAATAVQSNVAAQSPFVLOFQGRITLGLNL 900
Oy 901 QYFDPHESLSLRSIHPIRGKNTSBRAPFVLTCTPDKSQVPTIDDDVAAEPMNEM 960
Db 901 QYFDPHESLSLRSIHPIRGKNTSBRAPFVLTCTPDKSQVPTIDDDVAAEPMNEM 960
Oy 961 ERNLAEKEDNVKSNMORASPDLSGTWYKLSPPKQYKIPCLEVVDNDIVAGQDMIEL 1020
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Oy 1021 MTVESASQRIELHNSRCFIESIRPALBELSKASVTKCSISKLELSAAEOELLTLPSLE 1080
Db 1021 MTVESASQRIELHNSRCFIESIRPALBELSKASVTKCSISKLELSAAEOELLTLPSLE 1080
Oy 1081 SLEVSQTIOSQDOIFPMLDKFLCKELSYDLEGNIVAFVIEEPPNHNMEKLLIOISA 1140
Db 1081 SLEVSQTIOSQDOIFPMLDKFLCKELSYDLEGNIVAFVIEEPPNHNMEKLLIOISA 1140
Oy 1141 EYDPSKLVKLIQNSPNLAVFLKCNFSDGSLMTLVASCKLITIKESDSFQAVPEVA 1200
Db 1141 EYDPSKLVKLIQNSPNLAVFLKCNFSDGSLMTLVASCKLITIKESDSFQAVPEVA 1200
Oy 1201 SLNPFISIKILNLEGQOPDEETSEKAYITLGSLSMLELIIPTDGGYRYVAKLIIQCCQ 1260
Db 1201 SLNPFISIKILNLEGQOPDEETSEKAYITLGSLSMLELIIPTDGGYRYVAKLIIQCCQ 1260
Oy 1261 QHCLRLVLSFEKTLINDSVVEIAKVAISGQFOKLLENLKLINHKITBEGYRNFQALDNM 1320
Db 1261 QHCLRLVLSFEKTLINDSVVEIAKVAISGQFOKLLENLKLINHKITBEGYRNFQALDNM 1320
Oy 1321 PNLQELDISRHEFTCTCAQATVYKLSQCVLRPLIRLNMKSLMLDDDTALANWNER 1380
Db 1321 PNLQELDISRHEFTCTCAQATVYKLSQCVLRPLIRLNMKSLMLDDDTALANWNER 1380
Oy 1381 HPOSKYTLIIQKMLPFSPPIQX 1403
Db 1381 HPOSKYTLIIQKMLPFSPPIQX 1403

```

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GN BIRC1B OR NAIP2 OR NAIP-RS6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99431676; Pubmed=10501978;
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct
RT functional transcripts.";
RL Mamm. Genome 10:1032-1035(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99315342; Pubmed=10384056;
RA Varugh Z., Diez B., Gros P., Mackenzie A.;
RT "cDNA cloning and the 5' genomic organization of Naip2, a candidate
RT gene for murine Legionella resistance.";
RL Mamm. Genome 10:761-763(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=129/Sv;
RX MEDLINE=99417674; Pubmed=10486205;
RA Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,
RA Kunkel L.M., Miller W., Dietrich W.F.;
RT "Comparative sequence analysis of the mouse and human Lgm1/SmA
RT interval.";
RL Genomics 60:137-151(1999).
RN [4]
RP SEQUENCE OF 82-168 FROM N.A.
RX STRAIN=129/Sv;
RX MEDLINE=97131520; Pubmed=8975718;
RA Scharf J.M., Damron D., Frieella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
RT within the Lgm1 critical interval and contains multiple copies of Naip
RT exon 5.";
RL Genomics 38:405-417(1996).
CC -!- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 NACHT domain.
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CC -----
DB EMBL; AF135489; AAD56761.1; -
DB EMBL; AF135490; AAD56762.1; -
DB EMBL; AF102871; AAC73002.1; -
DB EMBL; AF131205; AAD56759.1; -
DB EMBL; U66329; AAC52977.1; -
DB PIR; T42628; T42628.
DB HSSP; Q13490; 10BH.
DB MGD; MGI:1296226; Birc1b.
DB InterPro; IPR003593; AAA_ATPase.
DB InterPro; IPR001370; BIR.
DB InterPro; IPR007111; NACHT_NTPase.
DB Pfam; PF00653; BIR; 3.
DB SMART; SM00382; AAA; 1.
DB SMART; SM00238; BIR; 3.
DB PROSITE; PS01282; BIR_REPEAT_1; 2.
DB PROSITE; PS0143; BIR_REPEAT_2; 3.
DB PROSITE; PS50837; NACHT; 1.
DB Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 508 802 NACHT.

```

FT CONFLICT 377 377 D -> G (IN REF. 3).
 FT CONFLICT 403 403 L -> F (IN REF. 3).
 FT CONFLICT 478 478 L -> I (IN REF. 3).
 FT CONFLICT 540 540 N -> Y (IN REF. 3).
 FT CONFLICT 862 862 K -> N (IN REF. 3).
 FT CONFLICT 1079 1089 SD -> FN (IN REF. 3).
 FT CONFLICT 1089 1089 R -> C (IN REF. 3).
 FT CONFLICT 1115 1115 K -> E (IN REF. 3).
 FT CONFLICT 1122 1122 T -> A (IN REF. 3).
 FT CONFLICT 1136 1136 D -> E (IN REF. 3).
 FT CONFLICT 1157 1157 D -> E (IN REF. 3).
 FT CONFLICT 1167 1167 G -> R (IN REF. 3).
 FT CONFLICT 1271 1271 F -> C (IN REF. 3).
 SQ SEQUENCE 1447 AA; 164033 MW; 98FC6A73BAE60A2 CRC64;

Query Match
 Best Local Similarity 2.5%; Score 35; DB 1; Length 1447;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOFCGCGCTGAGWEGDDPKHAKMPKCEPL 227
 193 DTVOFCGCGCTGAGWEGDDPKHAKMPKCEPL 227

DB BIRG_MOUSE STANDARD; PRT; 1402 AA.
 ID BIRG_MOUSE
 AC Q9JIB3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis
 inhibitor protein 7).
 GN BIRG1G OR NAIP7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID:10090;
 RP SEQUENCE FROM N.A.
 RA MEDLINE:20414747; PubMed:10958627;
 RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.,
 "Genomic sequence analysis of the mouse Naip gene array.";
 RL Genome Res. 10:1095-1102(2000).
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
 SIGNALS.
 CC -1- SIMILARITY: Contains 3 BIR repeats.
 CC -1- SIMILARITY: Contains 1 NACHT domain.

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 CC EMBL: AF242433; AAF82749.1;
 CC HSSP: Q13490; IOBH.
 DR MGD: MGI:185826; Birc1g.
 DR InterPro: IPR001370; BIR.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00236; BIR; 3.
 DR PROSITE: PS01282; BIR_REPEAT_1; 2.
 DR PROSITE: PS50143; BIR_REPEAT_2; 3.
 DR PROSITE: PS50837; NACHT; 1.
 KW Apoptosis; Repeat; Multigene family.
 FT REPEAT 60 127 BIR 1.
 FT REPEAT 159 227 BIR 2.
 FT REPEAT 278 345 BIR 3.
 FT DOMAIN 464 759 NACHT.
 SO SEQUENCE 1402 AA; 159662 MW; CIDPFA35893E0D CRC64;

Query Match
 Best Local Similarity 1.7%; Score 24; DB 1; Length 1402;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 204 LGNWECDPKHAKMPKCEPL 227
 204 LGNWECDPKHAKMPKCEPL 227

DB BIR_MOUSE STANDARD; PRT; 1403 AA.
 ID BIR_MOUSE
 AC Q9JIB3; Q9JIB3; Q9JIB3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 1a (Neuronal apoptosis
 inhibitor protein 1).
 GN BIRG1A OR NAIP1 OR NAIP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID:10090;
 RP SEQUENCE FROM N.A.
 RA Varaghi Z., Korneluk R.G., Mackenzie A.E.,
 "Cloning and characterization of the multiple copies of the murine
 homologue of NAIP (neuronal apoptosis inhibitor protein).";
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBD databases.
 RN [2]
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE:99431676; PubMed:10501978;
 RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.,
 "The mouse Naip gene cluster on Chromosome 13 encodes several distinct
 functional transcripts.";
 RL Mamm. Genome 10:1032-1035(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE:20414747; PubMed:10958627;
 RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.,
 "Genomic sequence analysis of the mouse Naip gene array.";
 RL Genome Res. 10:1095-1102(2000).
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
 SIGNALS.
 CC -1- SIMILARITY: Contains 3 BIR repeats.
 CC -1- SIMILARITY: Contains 1 NACHT domain.

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 CC EMBL: AF007769; AAB69223.1;
 CC EMBL: AF135491; AAD56763.1;
 CC EMBL: AF242432; AAF82752.1;
 CC HSSP: Q13490; IOBH.
 DR MGD: MGI:1298223; Birc1a.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR001370; BIR.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00236; AAA; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 1.
 DR PROSITE: PS50143; BIR_REPEAT_2; 3.
 DR PROSITE: PS50837; NACHT; 1.
 KW Apoptosis; Repeat; Multigene family.
 FT REPEAT 60 127 BIR 1.
 FT REPEAT 159 227 BIR 2.

```

FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 758 NACHT.
FT CONFLICT 343 343 I -> V (IN REF. 2).
FT CONFLICT 359 359 L -> Q (IN REF. 2).
FT CONFLICT 624 624 E -> K (IN REF. 2).
FT CONFLICT 1092 1092 D -> E (IN REF. 3).
FT CONFLICT 1116 1116 D -> N (IN REF. 3).
FT CONFLICT 1123 1123 G -> R (IN REF. 3).
FT CONFLICT 1129 1129 L -> H (IN REF. 1).
FT CONFLICT 1140 1140 T -> M (IN REF. 2).
FT CONFLICT 1269 1269 A -> V (IN REF. 3).
SQ SEQUENCE 1403 AA; 158692 MW; B31630259595E867 CRC64;

Query Match 1.7%; Score 24; DB 1; Length 1403;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 204 LGNMBGDDPMKSHAKMPKCEFL 227
Db 204 LGNMBGDDPMKSHAKMPKCEFL 227

RESULT 5
BIRF_MOUSE STANDARD; PRT; 1403 AA.
ID BIRF_MOUSE 090121; 009122; P81703; Q9R029;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1e (Neuronal apoptosis
inhibitory protein 5).
NC BIRCLF OR NAIP5 OR NAIP-RS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RA MEDLINE=99413676; PubMed=10501978;
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct
functional transcripts."
RL Mamm. Genome 10:1032-1035(1999).
[2]
SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA MEDLINE=99417674; PubMed=10486205;
RA Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,
RA Kunzel L.M., Miller W., Dietrich W.F.;
RT "Comparative sequence analysis of the mouse and human Lgnl/SMA
interval."
RL Genomics 60:137-151(1999).
[3]
SEQUENCE OF 82-168 FROM N.A.
RC STRAIN=129/SV;
RA MEDLINE=97131520; PubMed=8975718;
RA Scharf J.M., Damron D., Friessella A., Bruno S., Beggs A.H.,
RA Kunzel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
within the Lgnl critical interval and contains multiple copies of Naip
exon 5."
RL Genomics 38:405-417(1996).
-!- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
SIGNALS.
-!- SIMILARITY: Contains 3 BIR repeats.
-!- SIMILARITY: Contains 1 NACHT domain.
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CC -----
DR EMBL; AF135492; AAD56764.1; -.
DR EMBL; AF131205; AAD56760.1; -.
DR EMBL; U66326; AAC52974.1; -.
DR HSSP; Q13490; 10BH.
DR MGD; MGI:1298220; Bircle.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR007111; NACHT_NTPase.
DR Pfam; PF00653; BIR_3.
DR SMART; SM00238; BIR_3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS01443; BIR_REPEAT_2; 3.
DR PROSITE; PS50837; NACHT; 1.
KV Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 1.
FT REPEAT 278 345 BIR 2.
FT REPEAT 464 759 BIR 3.
FT DOMAIN 464 759 NACHT.
FT CONFLICT 92 92 K -> R (IN REF. 1).
FT CONFLICT 144 144 S -> R (IN REF. 1).
FT CONFLICT 242 242 T -> G (IN REF. 2).
FT CONFLICT 472 472 T -> A (IN REF. 2).
FT CONFLICT 516 516 A -> D (IN REF. 2).
FT CONFLICT 521 521 V -> T (IN REF. 2).
FT CONFLICT 533 533 V -> A (IN REF. 2).
FT CONFLICT 538 538 S -> I (IN REF. 2).
FT CONFLICT 1092 1092 E -> D (IN REF. 2).
FT CONFLICT 1129 1129 H -> L (IN REF. 2).
FT CONFLICT 1137 1137 R -> Q (IN REF. 2).
FT CONFLICT 1242 1242 V -> I (IN REF. 2).
FT CONFLICT 1276 1276 D -> N (IN REF. 2).
SQ SEQUENCE 1403 AA; 159695 MW; B27645043BC642 CRC64;

Query Match 1.7%; Score 24; DB 1; Length 1403;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 204 LGNMBGDDPMKSHAKMPKCEFL 227
Db 204 LGNMBGDDPMKSHAKMPKCEFL 227

RESULT 6
BIRF_MOUSE STANDARD; PRT; 1403 AA.
ID BIRF_MOUSE 090121; 009122; P81704;
AC 09JIB6; 009121; 009122; P81704;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1f (Neuronal apoptosis
inhibitory protein 6).
NC BIRCLF OR NAIP6 OR NAIP-RS4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RA MEDLINE=20414747; PubMed=10958627;
RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array."
RL Genome Res. 10:1095-1102(2000).
[2]
SEQUENCE OF 82-168 FROM N.A.
RC STRAIN=129/SV;
RA MEDLINE=97131520; PubMed=8975718;
RA Scharf J.M., Damron D., Friessella A., Bruno S., Beggs A.H.,
RA Kunzel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
within the Lgnl critical interval and contains multiple copies of Naip
exon 5."
RL Genomics 38:405-417(1996).

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CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 NACHT domain.
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CC -----
CC EMBL: AF242431; AAF82751.1; -
CC DR EMBL: U66327; AAC52975.1; -
CC DR HSP: MG1:129822; Birc1f.
CC DR MGD: MG1:129822; Birc1f.
CC DR InterPro: IPR001370; BIR.
CC DR Pfam: PF00653; BIR; 3.
CC DR SMART: SM00238; BIR; 3.
CC DR PROSITE: PS01282; BIR_REPEAT_1; 2.
CC DR PROSITE: PS50143; BIR_REPEAT_2; 3.
CC DR PROSITE: PS50837; NACHT; 1.
CC KW Apoptosis; Repeat; Multigene family.
CC FT REPEAT 60 127 BIR 1.
CC FT REPEAT 159 227 BIR 2.
CC FT REPEAT 278 345 BIR 3.
CC FT DOMAIN 464 759 NACHT.
CC SQ SEQUENCE 1403 AA; 159823 MW; 9D491250358C4F9 CRC64;

Query Match
Best Local Similarity 1.7%; Score 24; DB 1; Length 1403;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 LGNMGDDPMKHAHAKMPKCEPL 227
Db 204 LGNMGDDPMKHAHAKMPKCEPL 227

RESULT 7
ID NUSB_MYCTU STANDARD; PRT; 156 AA.
AC P95020;
DT 30-MAY-2000 (Rel. 39, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE N utilization substance protein B homolog (NusB protein).
GN NUSB OR RV2533C OR MT2608 OR MTCY159.23.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteriae; Actinobacteriales; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OC NCBI_taxonomy:1773;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE:98295987; PubMed:9634230;
RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornby T., Jorgensen K., Kroll M.A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Sanger S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sullivan J.S., Taylor K., Whitehead S., Barrett B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RA complete genome sequence.";
RA Nature 393:537-544(1998).
RA (2)
RP SEQUENCE FROM N.A.
RC STRAIN: CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

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RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Ueberbach T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains";
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RX MEDLINE:20343008; PubMed:1081194;
RA Gopal B., Haire L.F., Cox R.A., Colston M.J., Major S.,
RA Brannigan J.A., Smerdon S.J., Dodson G.;
RA "The crystal structure of NusB from Mycobacterium tuberculosis.";
RA Nat. Struct. Biol. 7:475-478(2000).
CC -1- FUNCTION: INVOLVED IN THE TRANSCRIPTION TERMINATION PROCESS
CC (BY SIMILARITY).
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: BELONGS TO THE NUSB FAMILY.
CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 144.
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CC -----
CC EMBL: Z63863; CAB06175.1; -
CC DR EMBL: AE007097; AAK46918.1; ALT_FRAME.
CC DR PIR: A70658; A70658.
CC DR PDB: 1EYV; 29-NOV-00.
CC DR TIGR: MT2608; -
CC DR TubercuList; RV2533c; -
CC DR HAMAP; MF 00073; -1;
CC DR InterPro: IPR006027; NusB.
CC DR Pfam: PF01029; NusB; 1.
CC KW Transcription termination; RNA-binding; 3D-structure;
CC Complete proteome.
CC FT HELIX 10 27
CC FT TURN 28 29
CC FT TURN 31 44
CC FT HELIX 46 47
CC FT TURN 53 64
CC FT HELIX 65 65
CC FT HELIX 66 74
CC FT TURN 75 76
CC FT TURN 78 79
CC FT HELIX 82 84
CC FT HELIX 87 102
CC FT TURN 104 105
CC FT HELIX 108 122
CC FT TURN 125 126
CC FT HELIX 127 156
CC SQ SEQUENCE 156 AA; 16740 MW; 84923E642CA5PD15 CRC64;

Query Match
Best Local Similarity 0.6%; Score 8; DB 1; Length 156;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AVOLAKEL 38
Db 115 AVOLAKEL 122

RESULT 8
ID OPLA_HUMAN STANDARD; PRT; 179 AA.
AC O14841;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 5-oxoprolinase (EC 3.5.2.9) (5-oxo-L-proline) (Pyroglutaminase)

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DE (5-Opase) (Fragment).
GN OPLAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA DeBelle L.R., Wood S.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: CATALYZES THE CLEAVAGE OF 5-OXO-L-PROLINE TO FORM L-
CC GLUTAMATE COUPLED TO THE HYDROLYSIS OF ATP TO ADP AND INORGANIC
CC PHOSPHATE.
CC -1- CATALYTIC ACTIVITY: ATP + 5-oxo-L-proline + 2 H(2)O = ADP +
CC phosphate + L-glutamate.
CC -1- SUBUNIT: Homodimer (by similarity).
CC -1- SIMILARITY: BELONGS TO THE OXOPROLINASE FAMILY.
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-----
DR EMBL; AF024673; AAB81519.1; -.
DR EMBL; AF024672; AAB81519.1; JOINED.
DR Genew; HGNC:8149; OPLAH.
DR MIM; 260005; -.
DR InterPro; IPR003692; Hydantoinase_B.
DR Pfam; PF02538; Hydantoinase_B; 1.
DR KX Hydrolase.
FT NON_TER 1 179
FT NON_TER 1 179
SQ SEQUENCE 179 AA; 19334 MW; BA13A42FECABEE8E CRC64;

Query Match 0.6%; Score 8; DB 1; Length 179;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 PEVFNQNLN 463
DB 101 PEVFNQNLN 108

RESULT 9
DNR1_STRPE STANDARD; PRT; 272 AA.
ID DNR1_STRPE
AC P25047.
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Regulatory protein dnr1.
GN DNR1.
OS Streptomyces peucetius.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCB1_TaxID=1950;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 29050;
RX MEDLINE=92104954; PubMed=1729206;
RA Stutzman-Engvall K.J., Otten S.L., Hutchinson C.R.;
RT "Regulation of secondary metabolism in Streptomyces spp. and
RT overproduction of daunorubicin in Streptomyces peucetius.";
RL J. Bacteriol. 174:144-154(1992).
CC -1- FUNCTION: MAY FORM, WITH DNR2 A TWO-COMPONENT REGULATORY SYSTEM
CC FOR DAUNORUBICIN BIOSYNTHESIS GENES.
CC -1- SIMILARITY: BELONGS TO THE APSR/DNR1/REDD FAMILY OF REGULATORS.
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DR EMBL; M80237; AAA26736.1; -.
DR PIR; A43306; A43306.
DR InterPro; IPR005158; BAD.
DR InterPro; IPR001867; Trans_reg_C.
DR Pfam; PF03704; BTAD; 1.
DR Pfam; PF00486; Trans_reg_C; 1.
DR ProDom; PD000329; Trans_reg_C; 1.
DR KX Antibiotic biosynthesis; Transcription regulation; DNA-binding.
SQ SEQUENCE 272 AA; 29698 MW; 97B59E1175030D93 CRC64;

Query Match 0.6%; Score 8; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LPELSAL 26
DB 185 LPELSAL 192

RESULT 10
ID YAS7_METUA STANDARD; PRT; 290 AA.
AC Q58457;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative glycosyl transferase MJ1057 (EC 2.-.-.-).
GN MJ1057.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCB1_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337959; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayon R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reisch C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Furumann J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
-----
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-----
DR EMBL; U67549; AAB99061.1; -.
DR HSP; P39621; 10GQ.
DR TIGR; MJ1057; -.
DR InterPro; IPR001173; Glyco_trans_2.
DR Pfam; PF00535; Glycos_transf_2; 1.
DR KX Hypothetical protein; Transferase; Complete proteome.
SQ SEQUENCE 290 AA; 35099 MW; 3F6A1B21C420D74 CRC64;

Query Match 0.6%; Score 8; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 12;

```

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1366 LDADDIAL 1373
 DB 97 LDADDIAL 104

RESULT 11
 FASH_RHOCA STANDARD; PRT; 324 AA.
 ID FASH_RHOCA STANDARD; PRT; 324 AA.
 AC P30790;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.41) (Beta-
 ketoadacyl-ACP synthase III) (KAS III).
 CM FASH.
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Rhodospirillaceae; Rhodospirillaceae;
 OX NCBI_TaxID=1061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92073365; PubMed=1961742;
 RA Toussein B., Boer C., Richard P., Colbeau A., Vignat P.M.,
 RT host factor in a Rhodospirillum rubrum gene encoding an integration
 RT host factor-like protein impairs in vivo hydroxylase expression.
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10749-10753(1991).
 CC -1- FUNCTION: CATALYZES THE CONDENSATION REACTION OF FATTY ACID
 CC FROM MALONYL-ACP. KAS III CATALYZES THE FIRST CONDENSATION
 CC REACTION WHICH INITIATES FATTY ACID SYNTHESIS AND MAY THEREFORE
 CC PLAY A ROLE IN GOVERNING THE TOTAL RATE OF FATTY ACID PRODUCTION.
 CC POSSESSES BOTH ACETOACETYL-ACP SYNTHASE AND ACETYL TRANSACYLASE
 CC ACTIVITIES (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-
 CC carrier protein] = 3-oxoacyl-[acyl-carrier protein] + CO(2) +
 CC [acyl-carrier protein].
 CC -1- PATHWAY: Fatty acid biosynthesis.
 CC -1- SIMILARITY: BELONGS TO THE FASH FAMILY.
 CC -----
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 CC -----
 CC DR EMBL, M84030; AAA26127.1;
 CC DR PIR, C41608; C41608.
 CC DR HSPB, P24245; 1HNK.
 CC DR InterPro: IPR004655; FASH.
 CC DR TIGRFAMs: TIGR00747; fash; 1.
 CC KM Fatty acid biosynthesis; Transferrase; Acyltransferase;
 CC FT ACT SITE 114 114 BY SIMILARITY.
 CC FT ACT SITE 251 251 BY SIMILARITY.
 CC FT ACT SITE 281 281 BY SIMILARITY.
 CC SO SEQUENCE 324 AA, 33732 MW, 730389857655202 CRC64,
 Query Match 0.6% Score 8; DB 1; Length 324;
 Blast Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 297 AALAKAGL 304
 DB 233 AALAKAGL 240
 RESULT 12
 SPPA_BACSU STANDARD; PRT; 335 AA.
 ID SPPA_BACSU STANDARD; PRT; 335 AA.

AC 034525;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative signal peptide peptidase sppa (EC 3.4.21.-).
 CM SPPA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=168;
 RX MEDLINE=98048467; PubMed=9387221.
 RA Lepidus A., Gallerton N., Sorokin A., Ehrlich S.D.,
 RT "Sequencing and functional annotation of the Bacillus subtilis genes
 RT in the 200 kb rmp-dnaB region."
 RL Microbiology 143:3431-3441(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Berteiro M.G., Bessieres P., Boloitin A., Borchert S.,
 RA Borries R., Bouteiller L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Dentzot F., Devine K.M., Duerksen A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabeet C., Ferrari B., Foulger D.,
 RA Fritz C., Fujita Y., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaeser P., Goffeau A., Goldlighty E.J., Grandi A.,
 RA Guteppl G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Iyaya M., Jones L.,
 RA Joris B., Katamata D., Kashiwara Y., Kleier-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetler P., Koningsreth G., Krogh S., Kumano M.,
 RA Kurita K., Lepidus A., Lardinois S., Lauber U., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Malet C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogawa A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Portetelle G., Prescott A.M.,
 RA Prescan E., Puig P., Fumelle B., Rapoport G., Ray M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadele Y.,
 RA Sato T., Scanlan B., Schleich S., Schroeter R., Scofield F.,
 RA Setoguchi J., Sekowaka A., Seror S.J., Seror P., Shin B.S., Solio B.,
 RA Setokhin A., Taccioni E., Takagi T., Takahashi H., Tkenari K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terstra P., Tognoni K.,
 RA Toseo V., Uchiyama S., Vandenbol M., Vannier P., Vassaret A.,
 RA Viart A., Wambut R., Wedler E., Wedler H., Weizenegger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasuno K., Yata K.,
 RA Yoshida K., Yoshikawa H.P., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis."
 RL Nature 390:249-256(1997).
 RN [3]
 RP FUNCTION.
 RP STRAIN=168;
 RX MEDLINE=93986931; PubMed=10455123;
 RX Bolhuis A., Matzen A., Hyyrylaenen H.-L., Kontinen V.P., Meina R.,
 RA Chapuis J., Venema G., Bron S., Frendl R., van Dijk J.M.,
 RT "Signal peptide peptidase- and ClpP-like proteins of Bacillus subtilis
 RT required for efficient translocation and processing of secretory
 RT proteins."
 RL J. Biol. Chem. 274:24585-24592(1999).
 CC -1- FUNCTION: DIGESTION OF THE CLEAVED SIGNAL PEPTIDES (BY
 CC SIMILARITY). REQUIRED FOR EFFICIENT PROCESSING OF PRECURSORS UNDER
 CC CONDITIONS OF HYPER-SECRETION.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S49.
 CC -----
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CC -----
CC EMBL; AF008820; AAC00312.1; -.
CC EMBL; Z99119; CAB14931.1; -.
CC PIR; B69990; B69990.
CC MEROPS; S49.001; -.
CC Subtilisin; B013839; sppsA.
CC InterPro; IPR002142; Peptidase_U7.
CC InterPro; IPR004635; SigPase_SppsA36.
CC Pfam; PF01343; Peptidase_U7; 1.
CC ProDom; PD002897; Peptidase_U7; 1.
CC TIGRfams; TIGR00706; SppA_dom; 1.
CC Hydrolase; Protease; Transmembrane; Complete proteome.
CC TRANSMEM 6 26 POTENTIAL.
CC SEQUENCE 335 AA; 36673 MW; 10BDA2DF8527D28B CRC64;

Query Match 0.6%; Score 8; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1082 LEVSGTQ 1089
Db 63 LEVSGTQ 70

RESULT 13
KCI METAN STANDARD; PRT; 382 AA.
AC 014408;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase (EC 2.7.1.12).
OS Metarhizium anisopliae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocnemycetidae; Hypocreales; Clavicipitaceae;
OC mitosporic Clavicipitaceae; Metarhizium.
OX NCBI_TaxID=5530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ME1 / ARSEF 2575; Bidochka M.J., Roberts D.W.;
RA Joseph L., St. Leger R.J., to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -----
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CC -----
CC EMBL; U28358; AAB80685.1; -.
CC HSSP; Q63450; 1A06.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0220; S_TGc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR TRANSFERase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding.
FT DOMAIN 23 278 PROTEIN KINASE.
FT NP BIND 29 37 ATP (BY SIMILARITY).
FT BINDING 50 50 ATP (BY SIMILARITY).
FT ACT SITE 142 142 BY SIMILARITY.
FT DOMAIN 291 301 CALMODULIN-BINDING (BY SIMILARITY).
SQ SEQUENCE 382 AA; 43532 MW; 9DA32959F4CA35E0 CRC64;

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Query Match 0.6%; Score 8; DB 1; Length 382;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 16 DHNLPEL 23
Db 285 DHNLPEL 292

RESULT 14
SAHH_PYRFU STANDARD; PRT; 421 AA.
AC SAHH_PYRFU
ID PS0251;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine
DE hydrolase) (AdoHcyase).
GN AHcy OR PF0343.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vci / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RA Chan M.K.S., Mukund S., Kletzin A., Adams M.W.W., Rees D.C.;
RT "Structure of a hyperthermophilic tungstopterin enzyme, aldehyde
RT ferredoxin oxidoreductase."
RL Science 267:1463-1469(1995).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
CC + L-homocysteine.
CC -1- COFACTOR: NAD (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the adenosylhomocysteinase family.
CC -----
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CC -----
CC EMBL; AE010158; AAL0467.1; -.
CC EMBL; X79777; CA56173.1; -.
DR HAMAP; H00563; -.
DR HAMAP; P10760; 1B3R.
DR InterPro; IPR000043; Ado_hcyase.
DR Pfam; PF05221; AdoHcyase; 1.
DR Pfam; PF00670; AdoHcyase; 1.
DR TIGRfams; TIGR00936; ahcy; 1.
DR PROSITE; PS00738; ADOHCYASE_1; 1.
DR PROSITE; PS00739; ADOHCYASE_2; 1.
DR Hydrolase; NAD; One-carbon metabolism; Complete proteome.
KW NP BIND 211 242 NAD (POTENTIAL).
FT SEQUENCE 421 AA; 47383 MW; 4ED68F6313CB412B CRC64;

Query Match 0.6%; Score 8; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 296 VAAKAG 303
Db 296 VAAKAG 303

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Db 89 VAALAKAG 96

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RESULT 15
SAHH_PVRHO
ID SAHH_PVRHO STANDARD; PRT; 421 AA.
AC 058275;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adenosylhomocysteinease (EC 3.1.1) (S-adenosyl-L-homocysteine
hydrolyase) (AdHcyase).
GN AHcy OR PHO540.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=96344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kozugi H., Hosoya A., Nagai Y.,
RA Sasaki M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohnuki Y.,
RA Funahashi T., Tanaka F., Kudo Y., Yamazaki U., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.,
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Rep. 5:55-76(1998).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
+ L-homocysteine.
CC -1- COFACTOR: NAD (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the adenosylhomocysteinease family.
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DR EMBL, AP000002; BAA29629.1; ALT_INIT.
DR HAMAP, MF_00563; -1.
DR HAMAP, PI0760; 1B3R.
DR InterPro: IPR000043; Ado_hcyase.
DR Pfam: PF05221; Adohcyase.1.
DR TIGRFAM: TIGR00936; ahcy.1.
DR PROSITE, PS00738; ADHCHYASE.1.1.
DR PROSITE, PS00739; ADHCHYASE.2.1.
KW Hydrolyase; NAD; One-carbon metabolism; Complete proteome.
NP BIND 211 242 NAD (POTENTIAL).
SQ SEQUENCE 421 AA; 47273 MW; 6BEB04955B5D951E CRC64;

Query Match 0.6%; Score 8; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 296 VAALAKAG 303
Db 89 VAALAKAG 96

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable general secretion pathway protein A.
GN GSPA OR B3323.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blotner F.R., Plunkett G., II, Bloch C.A., Perna N.T., Burland V.,
RA Bleyer M., Colado-Vides J., Glaeser J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
CC -1- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE
CC EXPORT OF PROTEINS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE EXPA FAMILY.
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DR EMBL, U18997; AA58120.1; -.
DR EMBL, AE000409; AAC76348.1; -.
DR PIR, P65125; P65125.
DR EcoGene; EG12888; GSPA.
KW Transport; ATP-binding; Complete proteome.
NP BIND 26 33
SQ SEQUENCE 489 AA; 55298 MW; 7C7DB828274E15C CRC64;

Query Match 0.6%; Score 8; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 470 GERGSGKT 477
Db 26 GERGSGKT 33

RESULT 17
BIR4 MOUSE
ID BIR4 MOUSE STANDARD; PRT; 496 AA.
AC 060989; 008865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacterial IAP repeat-containing protein 4 (Inhibitor of apoptosis
protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE BIR4 homolog A) (MIAP3) (MIAP-3).
GN BIR4 OR API3 OR XIAP OR ALPA OR MIHA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Pule K.L., Vaux D.L.,
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN (2)
RP SEQUENCE FROM N.A.
RA Farahani R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;

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RU Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
 CC (by similarity).
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
 CC inhibit apoptotic suppressor activity (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
 CC and -7, while the third BIR is involved in caspase-9 inhibition.
 CC The interactions with SMAC and PRSS25 are mediated by the second
 CC and third BIR domains (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: Contains 3 BIR repeats.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
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 CC -----
 CC EMBL: U36842; AAC52594.1; -
 CC EMBL: U88990; AAB58376.1; -
 CC HSSP: Q13490; IOBH.
 CC MGD: MGI:107572; Birc4.
 CC InterPro: IPR001370; BIR.
 CC InterPro: IPR001841; Znf_ring.
 CC Pfam: PF00653; BIR; 3.
 CC SMART: SM00238; BIR; 3.
 CC SMART: SM00184; RING; 1.
 CC PROSITE: PS01282; BIR_REPEAT_1; 3.
 CC PROSITE: PS50143; BIR_REPEAT_2; 3.
 CC PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 CC PROSITE: PS50089; ZF_RING_2; 1.
 CC KW Apoptosis; zinc-finger; Repeat.
 CC FT REPEAT 26 93 BIR 1.
 CC FT REPEAT 163 230 BIR 2.
 CC FT REPEAT 264 329 BIR 3.
 CC FT ZN FING 449 484 RING-TYPE.
 CC FT CONFLICT 208 208 E -> K (IN REF. 2).
 CC FT CONFLICT 317 317 E -> D (IN REF. 2).
 CC FT CONFLICT 322 322 W -> C (IN REF. 2).
 CC FT CONFLICT 346 346 S -> P (IN REF. 2).
 CC FT CONFLICT 360 360 I -> P (IN REF. 2).
 CC FT CONFLICT 388 388 I -> L (IN REF. 2).
 CC FT CONFLICT 449 449 C -> S (IN REF. 2).
 CC FT CONFLICT 462 462 V -> F (IN REF. 2).
 CC FT CONFLICT 468 468 V -> A (IN REF. 2).
 CC FT CONFLICT 490 490 K -> N (IN REF. 2).
 CC SQ SEQUENCE 496 AA; 56079 MW; EC5FAED0799F2CDD8 CRC64;
 Query Match 0.6%; Score 8; DB 1; Length 496;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 193 DTVOCFSC 200
 DB 59 DTVOCFSC 66
 AC Q9R0I6; STANDARD; PRT; 496 AA.
 ID BIR4_RAT
 RT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
 DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
 DE (IAP homolog A) (RIAP3) (RIAP-3).
 GN BIRC4 OR API3 OR XIAP.
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleota; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saito N.;
 RT "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA";
 RU Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
 CC (by similarity).
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
 CC inhibit apoptotic suppressor activity (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
 CC and -7, while the third BIR is involved in caspase-9 inhibition.
 CC The interactions with SMAC and PRSS25 are mediated by the second
 CC and third BIR domains (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: Contains 3 BIR repeats.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
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 CC -----
 CC EMBL: AB033366; BAA85304.1; -
 CC HSSP: Q13490; IOBH.
 CC InterPro: IPR001370; BIR.
 CC InterPro: IPR001841; Znf_ring.
 CC Pfam: PF00653; BIR; 3.
 CC SMART: SM00238; BIR; 3.
 CC SMART: SM00184; RING; 1.
 CC PROSITE: PS01282; BIR_REPEAT_1; 3.
 CC PROSITE: PS50143; BIR_REPEAT_2; 3.
 CC PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 CC PROSITE: PS50089; ZF_RING_2; 1.
 CC KW Apoptosis; zinc-finger; Repeat.
 CC FT REPEAT 26 93 BIR 1.
 CC FT REPEAT 163 230 BIR 2.
 CC FT REPEAT 264 329 BIR 3.
 CC FT ZN FING 449 484 RING-TYPE.
 CC SQ SEQUENCE 496 AA; 56072 MW; E250E3C77461A469 CRC64;
 Query Match 0.6%; Score 8; DB 1; Length 496;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 193 DTVOCFSC 200
 DB 59 DTVOCFSC 66
 ID AADS_EMER1
 AC P08158; STANDARD; PRT; 548 AA.
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Acetamidase (EC 3.5.1.4).
 GN AADS.
 OS Emeritella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichomycetaceae; Emeritella.
 OC NCBI_TaxID=162425;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87248110; Pubmed=3036667;
 RA Corrick C.M.; Twomey A.P.; Hynes M.J.;

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ACIN_RESULT 20
ACIN_MOUSE
ID ACIN_MOUSE STANDARD; PRT: 1338 AA.
AC 0901X; 09CSN7; 09CSR9; 09CSX7; 09R046; 09R047;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Apoptotic chromatin condensation inducer in the nucleus (Acinus).
ACINUS.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
(1)
SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
MEDLINE=99418559; PubMed=10490026;
Sahara S., Aceto M., Eguchi Y., Yamamoto N., Yoneda Y., Tsujimoto Y.;
"Acinus is a caspase-3-activated protein required for apoptotic
chromatin condensation."
Nature 401:166-173(1999).
(2)
SEQUENCE FROM N.A. (ISOFORM 1).
Mamoru A., Setsubo S., Yoshida T.;
"Whole-cloning of murine acinus1, a gene for apoptotic chromatin
condensation."
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
(3)
SEQUENCE OF 1-1190 FROM N.A. (ISOFORMS 1; 2 AND 4).
STRAIN=C57BL/6J; TISSUE=Embryo, and Pancreas;
MEDLINE=22354683; PubMed=12466851;
Okazaki Y., Furuno M., Kasukawa T., Adachi T., Bono H., Kondo S.,
Miyagi K., Tomaru Y., Hasegawa Y., Nogami H., Yamanaoka I., Kiyosawa H.,
Balderaselli R., Hill D.P., Bult C., Hume D.A., Queknebaugh J.,
Schmitt L.M., Karpman A., Matsuda H., Batalov S., Betsele K.W.,
Blake J.A., Bradt D., Brucic V., Chothia C., Corbani L.E., Cousins S.,

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RA Daille E., Dragani T.A., Fletcher C.F., Forrest A., Frizer K.S.,
RA Gasterlond T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmel S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltale L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavani W.D., Petrea G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Ring B.B., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Miyamoto L.G., Wyrnshaw-Borja A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carinici P., Hayatsu N.,
RA Hirozane-Kishikawa T., Komno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arahata T., Fukuda S.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Tsunemi E., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs." ;
RL Nature 420:563-573(2002).
CC -1- FUNCTION: Induces apoptotic chromatin condensation after
CC activation by CASP3 (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=L;
CC IsoId=Q9JIX8-1; Sequence=Displayed;
CC Name=2; Synonyms=S;
CC IsoId=Q9JIX8-2; Sequence=VSP_004030, VSP_004033;
CC Name=3; Synonyms=S';
CC IsoId=Q9JIX8-3; Sequence=VSP_004031;
CC Name=4;
CC IsoId=Q9JIX8-4; Sequence=VSP_004032;
CC -1- PTM: Undergoes proteolytic cleavage; the processed form is active,
CC -1- SIMILARITY: Contains 1 SAP domain.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
CC in position 110 and 112.
CC -----
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CC -----
DR EMBL: AF14725; AAD56723.1; -
DR EMBL: AF14729; AAD56727.1; -
DR EMBL: AF168782; AAF9661.1; ALT_PFRAME.
DR EMBL: AK011698; -, NOT ANNOTATED_CDS.
DR EMBL: AK012099; BAB28030.1; -
DR EMBL: AK012337; BAB28171.2; -
DR EMBL: AK050467; BAC34272.1; ALT_INIT.
DR GDB: MG1:1891824; Acinus.
DR GDB: GO:0005730; C:nucleolus.
DR InterPro: IPR000504; RNA_rec_mot.
DR InterPro: IPR003034; SAP.
DR SMART: SM00513; SAP; 1.
DR PROSITE: PS00800; SAP; 1.
DR Pfam: PF02037; SAP; 1.
DR KW Apoptosis; Nuclear protein; Alternative splicing.
FT DOMAIN 72 106 SAP.
FT DOMAIN 142 443 GLU-RICH.
FT DOMAIN 569 667 SEB-RICH.
FT DOMAIN 1131 1130 PRO-RICH.
FT SITE 1093 1094 ARB/ASP/GLU/LYS-RICH.
FT SITE 1094 1094 CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT VARSPPLIC 1 757 Missing (in isoform 2).
FT /FTID=VSP_004030.

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FT  VARSPLIC 1 773 Missing (in isoform 3).
FT  VARSPLIC 164 204 /Frid=VSP_004031.
FT  VARSPLIC 758 766 EAAESEDENTHPEGVASLPPDFQSSINRPELSTHSPR
FT  VARSPLIC 758 766 -> G (in isoform 4).
FT  VARSPLIC 758 766 /Frid=VSP_004032.
FT  VARSPLIC 758 766 ESERHHTV -> MMSFSDSRAG (in isoform 2).
FT  VARSPLIC 758 766 /Frid=VSP_004033.
FT  VARSPLIC 244 244 T -> A (IN REF. 2).
FT  VARSPLIC 515 515 T -> A (IN REF. 2).
FT  VARSPLIC 536 536 F -> L (IN REF. 2).
FT  VARSPLIC 557 557 G -> D (IN REF. 2).
FT  VARSPLIC 568 568 H -> Y (IN REF. 2).
FT  VARSPLIC 599 599 V -> A (IN REF. 2).
FT  VARSPLIC 729 729 S -> I (IN REF. 2).
FT  VARSPLIC 757 757 L -> P (IN REF. 2).
FT  VARSPLIC 773 773 T -> A (IN REF. 1; AAD56723).
FT  VARSPLIC 829 829 MISSING (IN REF. 3; BAB28030).
FT  VARSPLIC 896 896 Q -> R (IN REF. 3; BAB28030).
FT  VARSPLIC 1035 1035 G -> R (IN REF. 3; BAB28030).
SQ  SEQUENCE 1338 AA; 150690 MW; B912D9CB5750FB64 CRC64;

Query Match 0.64; Score 8; DB 1; Length 1338;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEBOOKER 46
DB 1256 EEEBOOKER 1262

RESULT 21
ACIN_HUMAN STANDARD; PRT: 1341 AA.
ID ACIN_HUMAN Q9UCV3; Q9UCV3; Q9UCV2;
AC Q9UCV3; Q9UCV3; Q9UCV3; Q9UCV2;
DI 28-FEB-2003 (Rel. 41, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DI Apoptotic chromatin condensation inducer in the nucleus (Actinus).
DI ACINUS OR KIA0670.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3), PARTIAL SEQUENCE, FUNCTION,
RP AND MUTAGENESIS OF ASP-1093.
RX MEDLINE=99418558; PubMed=10490026;
RA Sahara S., Aoto M., Eguchi Y., Imamoto N., Yoneda Y., Tsujimoto Y.;
RT "Actinus is a caspase-3-activated protein required for apoptotic
RT chromatin condensation."
RT Nature 401:168-173(1999).
RL [2]
RN SEQUENCE FROM N.A. (ISOFORM 4).
RC TISSUE=Uterus;
RA Wamburt R., Heubner D., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Fetal brain;
RA Li W.B., Gruber C., Jeesee J., Polayes D.;
RL "Full-length cDNA libraries and normalization."
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 56-1341 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA MEDLINE=99403880; PubMed=9734811;
RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro."
RL DNA Res. 5:159-176(1998).
CC -!- FUNCTION: Induces apoptotic chromatin condensation after

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CC activation by CASP3.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=D;
CC IsoId=Q9UKV3-1; Sequence=Displayed;
CC Name=2; Synonyms=S;
CC IsoId=Q9UKV3-2; Sequence=VSP_004025, VSP_004028;
CC Name=3; Synonyms=S;
CC IsoId=Q9UKV3-3; Sequence=VSP_004026, VSP_004029;
CC Name=4;
CC IsoId=Q9UKV3-4; Sequence=VSP_004027;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- PTM: Undergoes proteolytic cleavage; the processed form is active,
CC contrary to the uncleaved form.
CC -!- SIMILARITY: Contains 1 SAP domain.
CC
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CC
CC EMBL; AF124726; AAD56724.1; -
CC EMBL; AF124727; AAD56725.1; -
CC EMBL; AF124728; AAD56726.1; -
CC EMBL; AL050382; CAB43681.1; -
CC EMBL; BX247975; CAD62309.1; -
CC EMBL; AB014570; BAA31645.2; -
CC Genew; HGNC:17066; ACINUS.
CC
CC MIM; 604562; -
CC InterPro; IPR000504; RNA_rec_mot.
CC InterPro; IPR003034; SAP.
CC Pfam; PF02037; SAP; 1.
CC SMART; SM00513; SAP; 1.
CC PROSITE; PS50800; SAP; 1.
CC KW Apoptosis; Nuclear protein; Alternative splicing.
CC
CC DOMAIN 72 106
CC FT 142 442
CC FT 573 676
CC FT 1131 1131
CC FT 1132 1341
CC FT 1093 1094
CC FT 1093 727
CC FT 1
CC FT 758
CC FT 1
CC FT 1152
CC FT 766
CC VARSPLIC 728 766
CC FT 766
CC VARSPLIC 759 766
CC FT 1093 1093
CC FT 139 139
CC CONFLICT 139 139
CC SEQUENCE 1341 AA; 151887 MW; 8FE286681F63AB5C CRC64;

Query Match 0.64; Score 8; DB 1; Length 1341;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEBOOKER 46
DB 1256 EEEBOOKER 1263

RESULT 22
DPO3_CLOPE

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ID DPO3 CLOPE STANDARD; PRT; 1449 AA.
AC ORXJ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
CN DNA polymerase III polC-type (EC 2.7.7.7) (polIII).
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shima T., Ohtani K., Hirakawa H., Oshima K., Yamashita A.,
  "Complete genome sequence of Clostridium perfringens, an anaerobic
  flesh-eater.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
RL
CC -1- FUNCTION: Required for replicative DNA synthesis. This DNA
CC polymerase also exhibits 3' to 5' exonuclease activity (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY. POLC
CC SUBFAMILY.
CC
CC -----
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CC -----
DR EMBL; AP003191; BABB1397.1; .
DR HAMAP; MF_00356; .; 1
DR InterPro; IPR006054; DnaQ.
DR InterPro; IPR006055; Exonuclease.
DR InterPro; IPR004013; PNP_C.
DR InterPro; IPR001411; PNP_N.
DR InterPro; IPR006308; PolC_gnam_pos.
DR Pfam; PF00929; Exonuclease; 1.
DR Pfam; PF02811; PNP_C; 1.
DR Pfam; PF02231; EXOIII; 1.
DR SMART; SM00479; EXOIII; 1.
DR SMART; SM00481; POLIITAC; 1.
DR TIGRFAMs; TIGR00573; dnaq; 1.
DR TIGRFAMs; TIGR01405; polC_gnam_pos; 1.
DR Trnstrfam; DNA-directed DNA polymerase; DNA replication; Hydroxylase;
KM Nuclease; Exonuclease; Complete proclease.
FT DOMAIN 435 598 EXONUCLEASE.
SQ SEQUENCE 1449 AA; 163627 MW; AE2AE2CEEDJ32B85 CRC64;
Query Match 0.6%; Score 8; DB 1; Length 1449;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 679 KATAELK 686
DB 584 KATAELK 591

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GN A54L OR SALPD.
OS Vaccinia virus (strain WR), and
OC Vaccinia virus (strain Copenhagen).
OC Virusae; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10254, 10249;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=WR;
RX MEDLINE=91259063; PubMed=2045793;
RA Smith G.L., Chan Y.S., Howard S.T.;
RT "Nucleotide sequence of 42 kbp of vaccinia virus strain WR from near
RL J. Gen. Virol. 72:1349-1376(1991).
RN (2)
RP SEQUENCE OF 1-81 FROM N.A.
RC STRAIN=WR;
RX MEDLINE=91111982; PubMed=1846491;
RA Howard S.T., Chan Y.S., Smith G.L.;
RT "Vaccinia virus homologues of the Shope fibroma virus inverted
RT terminal repeat proteins and a discontinuous ORF related to the tumor
RL necrosis factor receptor family.";
RN Virol. 180:633-647(1991).
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=Copenhagen;
RX MEDLINE=91021027; PubMed=2219722;
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
RA Paolletti E.;
RT "The complete DNA sequence of vaccinia virus.";
RN Virol. 179:247-266(1990).
RN (4)
RP COMPLETE GENOME.
RC STRAIN=Copenhagen;
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
RA Paolletti E.;
RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";
RN Virol. 179:517-563(1990).
CC
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CC -----
DR EMBL; M35027; AAA48187.1; .
DR EMBL; M58054; .; NOT_ANNOTATED_CDS.
DR PIR; B42523; B42523.
SQ SEQUENCE 90 AA; 10800 MW; F3F9E9CE5D3B608 CRC64;
Query Match 0.5%; Score 7; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1269 SFPTLLN 1275
DB 43-SFPTLLN 49

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RESULT 24
ID YS15 BORBU STANDARD; PRT; 98 AA.
AC P70841;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 11p0protein BBD15 precursor.
CN BBD15 OR CDS.
OR Borrelia burgdorferi ( Lyme disease spirochete).
OC Plasmid Ipi7 (linear 17 kb) (1916).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.

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OX NCB1_TaxID=139;
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=97086634; PubMed=6932323;
RA Barbour A.G., Carter C.J., Bundock V., Hinebusch J.;
RT "The nucleotide sequence of a linear plasmid of Borrelia burgdorferi
RT reveals similarities to those of circular plasmids of other
RT prokaryotes."
RL J. Bacteriol. 178:6635-6639 (1996).
RN (2)
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Castens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.F., Fleischmann R.D., Richardson D., Peterson J.,
RA Peterson J., Kellavagge A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Ullrich T., White L., Adams M.D., Gocayne J.D., Weidman J.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
RT burgdorferi."
RL Nature 390:580-586 (1997).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -1- SIMILARITY: STRONG, TO B. BURGDOFFERI BPF20.
CC -----
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CC -----
DR EMBL: U43414; AAB38559.1; -.
DR EMBL: AE000793; AAC66348.1; ALT_INIT.
DR TIGR: BBD15; -.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Plasmid; Hypothetical protein; Lipoprotein; Membrane; Signal;
KW Complete proteome.
FT SIGNAL 1 21
FT CHAIN 98 98
FT LIPID 22 22
FT LIPID 22 22
FT LIPID 22 22
SO SEQUENCE 98 AA; 11513 MW; F5B57A33ACFE41C6 CRC64;
Query Match 0.5%; Score 7; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 434 LGCDLSI 440
DB 20 LGCDLSI 26
RESULT 25
Y266 RICPR STANDARD; PRT; 106 AA.
AC 092D09;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein RP266.
GN RP266.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCB1_TaxID=782;
RN RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;

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RX MEDLINE=99039499; PubMed=9823893;
RA Anderson S.G.E., Zomorodipour A., Anderson J.O.,
RA Sicheitiz-Ponten T., Alsmark U.C.M., Podowski R.M., Naestlund A.K.,
RA Eriksen A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140 (1998).
CC -1- SIMILARITY: BELONGS TO THE UPF0091 FAMILY.
CC -----
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CC -----
DR EMBL: AJ235271; CAAL4728.1; -.
DR PIR: F71681; F71681.
DR InterPro: IPR005133; Phag_MnHg_YuEb.
DR Pfam: PF03334; Phag_MnHg_YuEb; 1.
DR TIGRFAMs: TIGR01300; CPA3_mnHg_phag; 1.
KW Hypothetical protein; Complete proteome.
SO SEQUENCE 106 AA; 11775 MW; FDD7B12887F165BF CRC64;
Query Match 0.5%; Score 7; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 477 TVLAKKI 483
DB 98 TVLAKKI 104
RESULT 26
Y266 MUSE STANDARD; PRT; 117 AA.
AC P56841;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TcL1B2 protein.
GN TcL1B2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN RP SEQUENCE FROM N.A.
RX MEDLINE=20056259; PubMed=10588720;
RA Hallas C., Pekarsky Y., Itoyama T., Varnum J., Bichi R.,
RA Rothstein J.L., Croce C.M.;
RT "Genomic analysis of human and mouse TcL1 loci reveals a complex of
RT tightly clustered genes."
RL Proc. Natl. Acad. Sci. U.S.A. 96:14418-14423 (1999).
CC -1- SIMILARITY: BELONGS TO THE TcL1 FAMILY.
CC -----
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CC -----
DR EMBL: AF195489; AAF12802.1; -.
DR MGD: MGI:1351609; TcL1B2.
DR InterPro: IPR004833; TcL1B.
DR Pfam: PF015575; TcL1B; 1.
KW Multigene family.
SO SEQUENCE 117 AA; 13672 MW; A6B0851165B9B0AA CRC64;
Query Match 0.5%; Score 7; DB 1; Length 117;

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Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 MAAGFY 87
Db 1 MAAGFY 7

RESULT 27
YPL4 ARATH STANDARD; PRT; 121 AA.
ID YPL4 ARATH
AC 09LY56;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Y1Pee-like protein ACJ955890.
GN AT3655890 OR F2X19.70.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
NCBI_Taxid=3702;
[1]
SEQUENCE FROM N.A.
RA STRAIN=CV, Columbia;
RX MEDLINE=21016720; PubMed=1130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansgorge W., Unseld M.,
RA Fattmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA De Simone V., Boutry M., Griuell L.A., Maché R., Pügdennech P.,
RA Wincker P., Cattoico L., Weissbach J., Robert C., Brodter P.,
RA Schaefer M., Meiller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Brfle H., Jordan N., Bangert S.,
RA Wedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hontschner K., Kauer G., Loehner T.-H., Nordalek G.,
RA Reichelt J., Scharte M., Schen O., Bagues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
RA de Haan W., Maestre A.C., Alcaraz J.-P., Cortes A., Casacuberta E.,
RA Montfort A., Argitlon A., Flores M., Liquori R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-N.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Talion L.J., Jenkin J.,
RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maltz R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Miltcher J., Sellers P., Gill J.B., Feldlyum T.V.,
RA Preuss C.M., Kaneke T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Saemoco S., Kimura T., Ideawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara T., Matsumoto M., Matsuda A., Muraki A.,
RA Nakayama S., Nakazaki N., Shimizu S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
RT "Sequence" and analysis of chromosome 3 of the plant Arabidopsis
thaliana.
RL Nature 408:820-822 (2000).
[2]
SEQUENCE FROM N.A.
RA STRAIN=CV, Columbia;
RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.,
RT "RKN Arabidopsis full length cDNA clones (RAFs) sequenced by the
SSP Consortium (Salk/Stanford/PGSC)."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
[3]
-1- SIMILARITY: BELONGS TO THE Y1Pee FAMILY.
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CC EMBL, AL163832; CAB8743.1;

DR EMBL, AY050951; AK93628.1;
DR EMBL, AY051443; AA014382.1;
DR PIR, T49201; T49201.
DR InterPro, IP004910; Y1Pee.
DR Pfam, PF03226; Y1Pee; 1.
KW Hypothetical protein.
SQ SEQUENCE 121 AA; 13592 MW; 108668E24450AB31 CRC64;

Query Match 0.5%; Score 7; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1109 VDEGNT 1115
Db 7 VDEGNT 13

RESULT 28
YHCB_ECOLI STANDARD; PRT; 134 AA.
ID YHCB_ECOLI
AC P39436;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yHCB.
GN YHCB OR B3233 OR C3987 OR Z4592 OR ECS4106.
OS Escherichia coli.
OS Escherichia coli O6, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_Taxid=562, 217992, 83334;
[1]
SEQUENCE FROM N.A.
RA STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatter F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.,
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:12453-12474 (1997).
[2]
SEQUENCE FROM N.A.
RA STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G., III, Redford P., Roesech P.,
RA Raeko D., Buckles E.L., Ikon S.R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donenberg M.S., Schwartz D.C., Perna N.T.,
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
[3]
SEQUENCE FROM N.A.
RA STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Grobbeck B.J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Apolada J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blatter F.R.,
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533 (2001).
[4]
SEQUENCE FROM N.A.
RA STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shingawa H.,

RT "Complete genome sequence of enterohemorrhagic Escherichia coli
 RT 0157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 RM [5]
 RC SEQUENCE OF 10-134 FROM N.A.
 RC STRAIN-K12 / W3110;
 RA Baas S., Gu Q., Goddard A.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: STRONG, TO H. INFLUENZAE H1628.
 CC -----
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 CC -----
 CC EMBL; U18997; AAA58035.1; -;
 DR EMBL; AE000402; AAC76265.1; -;
 DR EMBL; AE016767; AAN82427.1; -;
 DR EMBL; AE005551; AAG58361.1; -;
 DR EMBL; AP002564; BAB37529.1; -;
 DR EMBL; U15661; -; NOT_ANNOTATED_CDS.
 DR PIR; B91142; B91142.
 DR PIR; G65115; G65115.
 DR PIR; E85987; E85987.
 DR Ecogene; EG12614; yhcB.
 DR Hypothetical protein; Complete proteome.
 SQ SEQUENCE 134 AA; 15239 MW; F357F30A599661B7 CRC64;
 OY Query Match 0.5%; Score 7; DB 1; Length 134;
 DB Best Local Similarity 100.0%; Pred. No. 64;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 19 LLEPLSA 25
 DB 86 LLEPLSA 92
 RESULT 29
 ID IL2_CAPRI STANDARD; PRT; 155 AA.
 AC P36835; P79156;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
 GN IL2.
 OS Capra hircus (Gcat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Ristved E.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Beyer J.C., Cheevers W.P.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
 CC MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-2 family.
 CC -----
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 CC -----
 CC EMBL; X76063; CAAS3664.1; -;
 DR EMBL; U34274; AAB38527.1; -;
 DR PIR; S38662; S38662.
 DR HSSP; P01585; 31NK.
 DR InterPro; IP800779; Interleukin-2.
 DR Pfam; PF00715; IL2; 1.
 DR PRINTS; PR00265; INTERLEUKIN2.
 DR ProDom; PD003649; Interleukin-2; 1.
 DR SMART; SM00189; IL2; 1.
 DR PROSITE; PS00424; INTERLEUKIN_2; 1.
 KM Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
 KM T-cell.
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 155 INTERLEUKIN-2.
 FT CATHOYD 23 123 O-LINKED (GALNAC. .) (BY SIMILARITY).
 FT DISULFID 79 127 BY SIMILARITY.
 FT CONFLICT 3 5 RMQ -> QIP (IN REF. 2).
 FT CONFLICT 22 22 P -> T (IN REF. 2).
 FT CONFLICT 30 30 T -> P (IN REF. 2).
 FT CONFLICT 51 51 L -> P (IN REF. 2).
 FT CONFLICT 71 71 D -> A (IN REF. 2).
 FT CONFLICT 89 89 D -> E (IN REF. 2).
 FT CONFLICT 99 99 R -> L (IN REF. 2).
 FT CONFLICT 107 113 YVASLKG -> SMQNIK (IN REF. 2).
 FT CONFLICT 140 140 Q -> L (IN REF. 2).
 FT CONFLICT 144 144 T -> I (IN REF. 2).
 FT CONFLICT 154 154 L -> M (IN REF. 2).
 SQ SEQUENCE 155 AA; 17703 MW; 90022DFB6AF78DB CRC64;
 OY Query Match 0.5%; Score 7; DB 1; Length 155;
 DB Best Local Similarity 100.0%; Pred. No. 72;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1294 LLENKLS 1300
 DB 51 LLENKLS 57
 RESULT 30
 ID YB43_MYCPN STANDARD; PRT; 175 AA.
 AC P75143;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MPN143 (E07_orf157).
 GN MPN143 OR MP011.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=87105885; PubMed=8948633;
 RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
 RL Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae".
 CC Nucleic Acids Res. 24:4420-4449(1996).
 CC -----
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 CC -----

CC -----
 DR EMBL: AF000002; AAB55659.1; -
 DR PIR: S73337; S73337.
 KM Hypothetical protein; Complete proteome
 SO SEQUENCE 175 AA; 20516 MW; 50DC73BF76335C0 CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 523 LEEKES 529
 DB 61 LEEKES 67

RESULT 31

DSBB_PASMTU STANDARD; PRT; 178 AA.
 ID DSBB_PASMTU STANDARD; PRT; 178 AA.
 AC Q9L6E3; P57804; -
 DT 15-OCT-2001 (Rel. 40, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Disulfide bond formation protein 8 (Disulfide oxidoreductase).
 GN DSBB OR PM0046.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Pasteurella.
 OX NCBI_TaxId=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fuller T.E., Kennedy M.J., Lowery D.E.;
 RT "Identification of Pasteurella multocida virulence genes in a
 RT septicemic mouse model using signature-tagged mutagenesis";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=pm70;
 RA MEDLINE=2145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida Pm70";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 CC -1- FUNCTION: Required for disulfide bond formation in some
 CC periplasmic proteins. Acts by oxidizing the dda protein (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (By similarity).
 CC -1- SIMILARITY: Belongs to the dsbb family.

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DR EMBL: AF237925; AAP68411.1; -
 DR EMBL: AE006038; AKK0130.1; -
 DR HAMAP: MF_00286; -1.
 DR InterPro: IPR003752; DdbB.
 DR Pfam: PF02600; DdbB.1.
 DR OxiReductase; Redox-active center; Transport; Electron transport;
 KM Chapterone; Transmembrane; Inner membrane; Complete proteome.
 FT TRANSMEM 1 14
 FT DOMAIN 31
 FT TRANSMEM 32 49
 FT TRANSMEM 50 65
 FT TRANSMEM 66 72
 FT TRANSMEM 73 90
 FT TRANSMEM 91 145
 FT TRANSMEM 146 164
 FT TRANSMEM 165 177
 FT DOMAIN 178
 FT DISULFID 44

FT DISULFID 105 131
 SO SEQUENCE 178 AA; 20036 MW; D2C45BB73B31F0BC CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1268 LSPFKTL 1274
 DB 2 LSPFKTL 8

RESULT 32

HP28_HUMAN STANDARD; PRT; 181 AA.
 ID HP28_HUMAN STANDARD; PRT; 181 AA.
 AC Q13442; Q92906; -
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 28 kDa heat- and acid-stable phosphoprotein (PDGF-associated protein)
 GN PDAP1 OR HASP28.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Neuroretina;
 RA MEDLINE=96373766; PubMed=8780057;
 RA Fischer W.H., Schubert D.;
 RT "Characterization of a novel platelet-derived growth factor-associated
 RT protein";
 RL J. Neurochem. 66:2213-2216(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Courtney L., Holmes A., Bauer C., Drone K.;
 RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Enhances PDGFA-stimulated cell growth in fibroblasts,
 CC but inhibits the mitogenic effect of PDGFB (By similarity).
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CC SEQUENCE OF 1-171 FROM N.A.
 CC Huang F.L.;
 CC Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Enhances PDGFA-stimulated cell growth in fibroblasts,
 CC but inhibits the mitogenic effect of PDGFB (By similarity).
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CC SEQUENCE OF 1-171 FROM N.A.
 CC Huang F.L.;
 CC Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Enhances PDGFA-stimulated cell growth in fibroblasts,
 CC but inhibits the mitogenic effect of PDGFB (By similarity).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U41745; AAC50452.1; -
DR EMBL; AC004922; AAF03506.1; -
DR EMBL; BC000684; AAH00684.1; -
DR EMBL; BC007873; AAH07873.1; -
DR EMBL; U65960; AAB07135.1; -
DR Genew; HGNC:14634; PDAP1.
DR MIM; 607075; -
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
KM Phosphorylation.
FT CONFLICT 1 1 M -> MI (IN REF. 4).
FT CONFLICT 13 13 R -> W (IN REF. 4).
FT CONFLICT 25 25 A -> T (IN REF. 4).
FT CONFLICT 29 29 A -> S (IN REF. 4).
FT CONFLICT 67 67 E -> D (IN REF. 4).
FT CONFLICT 80 80 L -> F (IN REF. 4).
FT CONFLICT 126 126 K -> R (IN REF. 4).
SO SEQUENCE 181 AA; 20630 MW; F97914C7920ABAB3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 181;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEEOKE 45
DB 36 EEEEOKE 42

RESULT 33
MPL_MPLV STANDARD; PRT; 184 AA.
ID PA0331:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Myeloproliferative leukemia protein.
GN V-MPL.
OS Myeloproliferative leukemia virus (MPLV).
OC Viruses; Retrovird viruses; Retroviridae.
OX NCBI_Taxid=11973;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91084843; PubMed=2175677;
RA Souyri M., Vigon I., Penciolelli J.-F., Heard J.-M., Tambourin P.,
RA Wendling F.;
RT A putative truncated cytokine receptor gene transduced by the
RT myeloproliferative leukemia virus immortalizes hematopoietic
RT progenitors."
RL Cell 63:1137-1147(1990).
CC -!- FUNCTION: TRUNCATED FORM OF THE RECEPTOR FOR THROMBOPOIETIN.
CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS AN ENV-MPL
CC POLYPEPTIDE.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL; M60350; AAA77654.1; -
DR HSSP; P19235; IERN.
DR InterPro; IPR003528; Hemopoipo_L_F1.
DR PROSITE; PS001352; HEMATOPO_REC_L_F1; PARTIAL.
KM Receptor; Transmembrane; Oncogene.
FT TRANSMEM 44 POTENTIAL.
SO SEQUENCE 184 AA; 20558 MW; 7956D3363940B735 CRC64;

```

Query Match Similarity 0.5%; Score 7; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 LSNLGL 29
Db 56 LSNLGL 62

RESULT 34
ID T2D9 DROME STANDARD; PRT; 196 AA.
AC P49566; OSV190;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transcription Initiation factor TFIIID 28 kDa subunit beta
DE (p28-beta) (TAFII30 beta).
GN TAFII OR TAF30-BETA OR CG4079.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Rhyngoteria; Drosophilidae; Drosophila.
CX NCBI_TaxID=1227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94102540; PubMed=8276241;
RA Yokomori K., Chen J.L., Admon A., Zhou S., Tjian R.;
RT Molecular cloning and characterization of dTAFII30 alpha and
RT dTAFII30 beta: two small subunits of Drosophila TFIIID."
RL Genes Dev. 7:2587-2597(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Nakatani Y.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA Manasteris P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Miller B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miles G.L.G.,
RA April J.F., Aggrey A.A., An H.-J., Andrews-Plamhoch C., Baldwin D.,
RA Ballew R.M., Bessu A.J., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benca P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brooks P., Brotler P.,
RA Burris K.C., Busan D.A., Butler E., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dong L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,
RA Giesler A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Idegawa C.,
RA Jajani M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mates J., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Mostrel A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
RA Shue B.C., Sidenkiamos I., Simpson M., Skupel M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svaykaba R., Tector C., Turner R., Venier B., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley C.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RT "The genome sequence of *Drosophila melanogaster*,"
 RL Science 287:2185-2195 (2000).
 CC -1- FUNCTION: TPID IS A MULTIMERIC PROTEIN COMPLEX THAT PLAYS A
 CC CENTRAL ROLE IN MEDIATING PROMOTER RESPONSES TO VARIOUS ACTIVATORS
 CC AND REPRESSORS.
 CC -1- SUBUNIT: TPID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A
 CC NUMBER OF TBP-ASSOCIATED FACTORS (TAFs).
 CC -1- SIMILARITY: BELONGS TO THE TAF21 FAMILY.
 CC -----
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 CC -----
 DR EMBL: S67660; AAB29541.1; -
 DR EMBL: U06457; AAB19245.1; -
 DR EMBL: A500362; AAF52806.1; -
 DR PIR: B49453; B49453.
 DR TRANSFAC: T02131; -
 DR Flybase: FBgn0011291; Taff1.
 DR InterPro: IPR004822; H1etong_core.
 DR InterPro: IPR006809; TAF128.
 DR Pfam: PF04719; TAF128; 1.
 DR Transcription regulation.
 FT DOMAIN
 SO SEQUENCE 196 AA; 22091 MW; E85285E3F598AC9 CRC64;
 Query Match
 Best Local Similarity 0.5%; Score 7; DB 1; Length 196;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 36 KELEEE 42
 DB 79 KELEEE 85

RESULT 35
 PSMB PYRAB STANDARD; PRT; 207 AA.
 ID PSMB PYRAB
 AC Q9V0N9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Proteasome beta subunit precursor (EC 3.4.25.1) (Multicatalytic
 DE endopeptidase complex beta subunit).
 GN PSMB OR PYRAB07500 OR PAH167.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 NCBI_TaxID=99232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GES / Orsay;
 RX PubMed=12622808;
 RA Cohen G.N., Barbe V., Plament D., Galperin M., Hellig R., Lecompte O.,
 RA Poch O., Prieur D., Querellon J., Ripp R., Thierry J.-C.,
 RA Van der Oost J., Weissbach J., Zivanovic Y., Forterre P.,
 RT "An integrated analysis of the genome of the hyperthermophilic
 RT archaeon *Pyrococcus abyssi*,"
 RL Mol. Microbiol. 47:1495-1512 (2003).
 CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
 CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
 CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
 CC NEUTRAL OR SLIGHTLY BASIC PH (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad
 CC specificity.

CC -1- SUBUNIT: COMPOSED OF TWO SUBUNITS, ALPHA AND BETA. THE COMPLEX IS
 CC FORMED OF FOUR RINGS. THE TWO OUTER RINGS ARE EACH COMPOSED OF
 CC SEVEN ALPHA SUBUNITS. THE TWO INNER RINGS ARE EACH COMPOSED OF
 CC SEVEN BETA SUBUNITS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to peptidase family T1B.
 CC -----
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 CC -----
 DR EMBL: AJ248285; CAB49664.1; -
 DR PIR: G75118; G75118.
 DR HSSP: P28061; IPMA.
 DR MEROPS: T01.002; -
 DR InterPro: IPR000243; Proteasome B.
 DR InterPro: IPR001353; Protease B.
 DR Pfam: PF00227; Proteasome; 1.
 DR PRINTS: PR00141; PROTEASOM.
 DR PROSITE: PS00894; PROTEASOM; B; 1.
 KM Proteasome; Hydrolyase; Protease; Complete proteome.
 FT PROPEP 1
 FT FT 10
 FT CHAIN 11 207 APPARENTLY REMOVED IN MATURE FORM (BY
 FT ACT SITE 11 11 PROTEASOME BETA SUBUNIT.
 FT FT PROBABLE.
 SO SEQUENCE 207 AA; 22671 MW; 9FBD9B0519434939 CRC64;
 Query Match
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1305 ITRBGR 1311
 DB 188 ITRBGR 194

RESULT 36
 DCL LYCES STANDARD; PRT; 224 AA.
 ID DCL LYCES
 AC Q42463;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE DCL protein, chloroplast precursor (Defective chloroplasts and leaves
 DE protein).
 GN DCL.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.
 NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV Moneymaker;
 RX MEDLINE=97015121; PubMed=8861949;
 RA Keddie J.S., Carroll B., Jones J.D.G., Grissam W.,
 RA "The DCL gene of tomato is required for chloroplast development and
 RA palisade cell morphogenesis in leaves,"
 RL EMBL J. 15:4208-4217 (1996).
 CC -1- FUNCTION: HAS A FUNCTION IN THE EARLY STAGE OF CHLOROPLAST
 CC DEVELOPMENT AND PALISADE CELL MORPHOGENESIS.
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -----
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CC -----

DR EMBL; U55278; AAC49434.1; -

DR EMBL; U55219; AAC49433.1; -

DR PIR; S71749; S71749.

KW Chloroplast; Transit peptide.

FT TRANSIT 1 50

FT CHAIN 51 224

FT DCL PROTEIN

SO SEQUENCE 224 AA; 25438 MW; 15703EF39F58179D CRC64;

Query Match 0.5%; Score 7; DB 1; Length 224;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 368 LETTSES 374

DB 74 LETTSES 80

RESULT 37

DAG_ANTMA STANDARD; PRT; 230 AA.

ID Q38732;

AC 15-JUL-1989 (Rel. 38, Created)

DT 15-JUL-1989 (Rel. 38, Last sequence update)

DT 15-JUL-1989 (Rel. 38, Last annotation update)

DS DAG protein, chloroplast precursor.

DAG:

OS Antirrhinum majus (Garden snapdragon).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; lamiales; Lamiales; Antirrhinaceae; Antirrhineae;

OC Antirrhinum

NCBI_TaxID=4151;

OX NCBI_TaxID=4151;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=leaf;

RX MEDLINE=97015120; PubMed=8861948;

RA Chatterjee M., Sparvoli S., Edmunds C., Garosi P., Findlay K., Martin C.;

RA "DAG, a gene required for chloroplast differentiation and palisade development in Antirrhinum majus";

RT development in Antirrhinum majus";

RL EMBD J. 15:4194-4207(1996).

CC -1- FUNCTION: ACTS VERY EARLY IN CHLOROPLAST DEVELOPMENT, BEING REQUIRED FOR EXPRESSION OF RNA POLYMERASE BETA SUBUNIT GENE, AND HENCE INDIRECTLY FOR SUBSEQUENT EXPRESSION OF CAB AND RBCS GENES.

CC -1- SUBCELLULAR LOCATION: Chloroplast.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN LEAVES, FLOWERS INCLUDING PETALS, AND TO A LOW LEVEL IN ROOTS.

CC -1- MISCELLANEOUS: EXPRESSION DETECTED IN THE DARK, BUT ENHANCED BY LIGHT.

CC -----

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CC -----

CC EMBL; X95753; CAA65064.1; -

DR PIR; S71747; S71747.

KW Chloroplast; Transit peptide.

FT TRANSIT 1 55

FT CHAIN 56 230

FT DOMAIN 66 71

FT POLY-ASN.

FT DCL PROTEIN.

SO SEQUENCE 230 AA; 25852 MW; CDB33CEBD0DD465 CRC64;

Query Match 0.5%; Score 7; DB 1; Length 230;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1221 ERTSEKF 1227

DB 145 ERTSEKF 151

RESULT 38

ID_ARAD_BACCH STANDARD; PRT; 231 AA.

AC O9K8Q4;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) (Phosphoribulose isomerase).

DR ARAD OR B11871.

GN ARAD Firmicutes; Bacillales; Bacillaceae; Bacillus.

OS Bacillus halodurans.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=86665;

OX NCBI_TaxID=86665;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C-125 / JCM 9153;

RX MEDLINE=20512582; PubMed=11058132;

RA Takami H., Nakaseone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kohara S., Horikoshi K.;

RA "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.";

RT Nucleic Acids Res. 28:4317-4331(2000).

RL -1- CATALYTIC ACTIVITY: L-ribulose 5-phosphate = D-xylulose 5-phosphate.

CC -1- COFACTOR: Binds one zinc ion per molecule (Potential).

CC -1- PATHWAY: L-arabinose catabolism; third step.

CC -1- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/FUCA SUBFAMILY.

CC -----

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CC -----

CC EMBL; AP001513; BAB05590.1; -

DR PIR; G838B3; G838B3.

DR InterPro; IPR001303; Aldolase_II_N.

DR Pfam; PF00596; Aldolase_II; 1.

KW Arabinose catabolism; Isomerase; Zinc; Complete proteome.

FT METAL 75 75

FT METAL 94 94

FT METAL 96 96

FT METAL 168 168

FT ZINC (BY SIMILARITY).

FT ZINC (BY SIMILARITY).

FT ZINC (BY SIMILARITY).

SO SEQUENCE 231 AA; 25991 MW; 6CA570D2A6BD97 CRC64;

Query Match 0.5%; Score 7; DB 1; Length 231;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1109 VDLEGT 1115

DB 59 VDLEGT 65

RESULT 39

ID_SRY_MOUSE STANDARD; PRT; 232 AA.

AC P13675;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Y-linked testis-specific protein.

GN SRY.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=87174820; PubMed=3562242;
 RA Bishop G.E., Hatac D.;
 RT "Molecular cloning and sequence analysis of a mouse Y chromosome RNA
 RT Nucleic Acids Res. 15:2959-2969(1987).
 CC -1- SIMILARITY: BELONGS TO THE SPIN / STSY FAMILY.
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 CC -----
 DR EMBL: X05260; CAA28881.1; -
 DR PIR: A27503; A27503.
 DR MGD: MGI:99467; Sny.
 DR InterPro: IPR003671; Spin_Sety.
 DR Pfam: PF02513; Spin_Sety; 3.
 KW Phosphorylation; Testis.
 FT MOD_RES 190 190
 FT MOD_RES 218 218
 FT MOD_RES 218 218
 SQ SEQUENCE 232 AA; 26796 MW; 52E898D5125548D6 CRC64;
 Query Match Best Local Similarity 0.5%; Score 7; DB 1; Length 232;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 549 LDDYKE 555
 DB 148 LDDYKE 154
 RESULT 40
 ID SPIN_HUMAN STANDARD; PRT; 232 AA.
 AC Q99865; Q99865; Q99865;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Spindlin homolog (Protein DXP34).
 GN DXP34.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97419273; PubMed=9271673;
 RA Laval S.H., Reed V., Blair H.J., Boyd Y.;
 RT "The structure of DXP34, a human X-linked sequence family with
 RT homology to a transcribed mouse Y-linked repeat."
 RT Mamm. Genome 6:689-691(1997).
 CC Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SPIN / STSY FAMILY.
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 CC -----

DR EMBL: Y09858; CAA70988.1; -
 DR EMBL: AL022157; CAA18148.1; -
 DR EMBL: AL022157; CAA18149.1; -
 DR GO: GO:0000725; P:development; ISS.
 DR GO: GO:0000745; P:regulation of cell cycle; ISS.
 DR InterPro: IPR003671; Spin_Sety.
 DR Pfam: PF02513; Spin_Sety; 3.
 KW Developmental protein; Phosphorylation; Cell cycle.
 FT MOD_RES 196 196
 FT MOD_RES 224 224
 FT MOD_RES 224 224
 FT MOD_RES 20 20
 FT MOD_RES 208 208
 FT MOD_RES 208 208
 SQ SEQUENCE 232 AA; 26536 MW; 093E7B9F540B71 CRC64;
 Query Match Best Local Similarity 0.5%; Score 7; DB 1; Length 232;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 549 LDDYKE 555
 DB 151 LDDYKE 157
 RESULT 41
 ID SPIN_HUMAN STANDARD; PRT; 237 AA.
 AC Q95671; Q95671; Q95671;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Spindlin (Ovarian cancer-related protein).
 GN SPIN OR OCR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=pituitary;
 RA Peng Y., Song H., Dai M., Huang Q., Mao Y., Zhang Q., Mao M., Fu G.,
 RA Luo M., Chen J., Hu R.;
 RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC SEQUENCE FROM N.A.
 RA Zhang H.L., Yu L., Wang X., Chen Z., Tu Q., Chen J.Q., Ding J.B.,
 RA Gao J., Zhao S.Y.;
 RT "Cloning, characterization and mapping of human SPIN to human
 RT chromosome 9q22.1-22.3."
 RT Chin. Sci. Bull. 45:909-914(2000).
 CC [3]
 CC Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROBABLY PLAYS A ROLE IN CELL-CYCLE REGULATION DURING
 CC THE TRANSITION FROM GAMETE TO EMBRYO (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SPIN / STSY FAMILY.
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 CC -----
 DR EMBL: AF106682; AAK43035.1; ALT_INIT.
 DR EMBL: AF087864; AAK48367.1; -
 DR EMBL: AF137228; AAK38112.1; -
 DR Genew: HGNC:11243; SPIN.
 DR InterPro: IPR003671; Spin_Sety.

DR Pfam: PF02513; Spin-Scty; 3.
 KM Developmental protein; Phosphorylation; Cell cycle.
 FT MOD_RES 201 201 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 229 229 PHOSPHORYLATION (POTENTIAL).
 SQ SEQUENCE 237 AA; 27077 MW; 92267246E98572CE CRC64;
 Query Match 0.5%; Score 7; DB 1; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 LDDYKE 555
 DB 156 LDDYKE 162

RESULT 42
 CALD_MEIGA STANDARD; PRT; 239 AA.
 AC P13505;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Caldesmon, smooth muscle (CDM) (Fragment).
 GN CALD1 OR CAD.
 OS Meleagris gallopavo (Common turkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archaeopteryx; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 OX NCBI_TaxID=9103;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Glizzard;
 RX MEDLINE=89273603; PubMed=2730648;
 RA Leszyk J., Mornet D., Audemard E., Collins J.H.;
 RT "Caldesmon structure and function: sequence analysis of a 35
 RT kilodalton actin- and calmodulin-binding fragment from the C-terminus
 RT of the turkey glizzard protein.";
 RL Biochem. Biophys. Res. Commun. 160:1371-1378(1989).
 [2]
 RP SEQUENCE OF 1-96.
 RC TISSUE=Glizzard;
 RX MEDLINE=89228015; PubMed=2653315;
 RA Leszyk J., Mornet D., Audemard E., Collins J.H.;
 RT "Amino acid sequence of a 15 kilodalton actin-binding fragment of
 RT turkey glizzard caldesmon: similarity with dystrophin, tropomyosin and
 RT the tropomyosin-binding region of tropomyosin T.";
 RL Biochem. Biophys. Res. Commun. 160:210-216(1989).
 CC -1- FUNCTION: CONTROL OF ACTOMYOSIN INTERACTIONS IN SMOOTH MUSCLE
 CC AND NONMUSCLE CELLS (COULD ACT AS A BRIDGE BETWEEN MYOSIN AND
 CC ACTIN FILAMENTS). INHIBITS THE ACTIN-ACTIVATED ATPASE OF MYOSIN
 CC THIS INHIBITION IS ATTENUATED BY CALCIUM-CALMODULIN AND IS
 CC POTENTIATED BY TROPOMYOSIN. INTERACTS WITH ACTIN, MYOSIN,
 CC 2 MOLECULES OF TROPOMYOSIN AND WITH CALMODULIN.
 CC -1- SUBCELLULAR LOCATION: ON THIN FILAMENTS IN SMOOTH MUSCLE AND ON
 CC STRESS FIBERS IN FIBROBLASTS (NONMUSCLE).
 CC PIR: S16925; S16925.
 DR InterPro: IPR006017; Caldesmon.
 DR InterPro: IPR006018; Caldesmon_LSP.
 DR Pfam: PF02029; Caldesmon_1.
 DR PRINTS: PRO1076; CALDESMON.
 KM Muscle protein; Actin-binding; Calmodulin-binding.
 FT NON TER 1 1
 FT MOD_RES 239 239
 FT NON TER 239 239
 SQ SEQUENCE 239 AA; 26561 MW; D395B8BB465B8895 CRC64;

Query Match 0.5%; Score 7; DB 1; Length 239;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 LEEBEOK 44
 DB 41 LEEBEOK 47

RESULT 43
 SPIN_MOUSE STANDARD; PRT; 240 AA.
 ID SPIN_MOUSE
 AC Q61142;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Spindlin (30000 Mr metaphase complex) (SSC P).
 GN SPIN.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X DBA/2; TISSUE=Embryo;
 RX MEDLINE=97178984; PubMed=9053325;
 RA Oh B., Hwang S.Y., Solter D., Knowles B.B.;
 RT "Spindlin, a major maternal transcript expressed in the mouse during
 RT the transition from oocyte to embryo.";
 RL Development 124:493-503(1997).
 CC -1- FUNCTION: PROBABLY PLAYS A ROLE IN CELL-CYCLE REGULATION DURING
 CC THE TRANSITION FROM GAMETE TO EMBRYO.
 CC -1- SUBCELLULAR LOCATION: ASSOCIATES WITH THE MEIOTIC SPINDLE.
 CC -1- TISSUE SPECIFICITY: OOCYTE, EGG, AND VERY EARLY EMBRYO; NOT IN THE
 CC 8-, AND 16-CELL STAGE OF THE EMBRYO. SYNTHESIZED FROM MATERNAL
 CC -1- DEVELOPMENTAL STAGE: GAMETOGENESIS.
 CC -1- PTM: PHOSPHORYLATION DURING OOCYTE MEIOTIC MATURATION.
 CC -1- PTM: POST-TRANSLATIONALLY MODIFIED DURING THE FIRST MITOTIC CELL
 CC CYCLE.

-1- SIMILARITY: BELONGS TO THE SPIN / STSY FAMILY.

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CC EMBL: U46972; AAA91233.1; -.
 DR MGD: MGI:109242; Spin.
 DR InterPro: IPR003671; Spin_Scty.
 DR Pfam: PF02513; Spin-Scty; 3.
 KM Developmental protein; Phosphorylation; Cell cycle.
 FT MOD_RES 204 204
 FT MOD_RES 232 232 PHOSPHORYLATION (POTENTIAL).
 SQ SEQUENCE 240 AA; 27136 MW; D46F03847B8C876 CRC64;

Query Match 0.5%; Score 7; DB 1; Length 240;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 LDDYKE 555
 DB 159 LDDYKE 165

RESULT 44
 CODY_CLOPE STANDARD; PRT; 258 AA.
 ID CODY_CLOPE
 AC O8XJ05;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE GTP-sensing transcriptional pleiotropic repressor cody.
 GN CODY OR CPE1701.
 OS Clostridium perfringens.
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 CC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]

RC STRAIN=13 / Type A;
 RX MEDLINE=21664373; PubMed=11792842;
 RA Shima T., Ohtani K., Hatakeyama H., Ohtsuka K., Yamashita A.,
 RT Complete genome sequence of *Clostridium perfringens*, an anaerobic
 RL flesh-eater".
 Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 CC -1- FUNCTION: DNA-binding protein that represses the expression of
 CC many genes that are induced as cells make the transition from
 CC rapid exponential growth to stationary phase (by similarity). It
 CC is a GTP-binding protein that senses the intracellular GTP
 CC concentration as an indicator of nutritional limitations. At low
 CC GTP concentration it no longer binds GTP and stop to act as a
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- SIMILARITY: Belongs to the cody family.
 CC -----
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 CC -----
 DR EMBL; AF003191; BAB1407.1; -.
 DR HAMAP; MF_00621; -1.
 KW Transcription regulation; Repressor; DNA-binding; GTP-binding;
 KW Complete proteome.
 FT DNA BIND 203
 SO SEQUENCE 258 AA; 28546 MW; E697D3570F83D111 CRC64;
 Query Match
 Best Local Similarity 0.5%; Score 7; DB 1; Length 258;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 706 ERNDDL 712
 DB 135 ERNDDL 141

RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Motley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz U., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalheuer D.E.,
 RA Schermer A., Schein J.E., Jones S.J.W., Marra M.A.,
 RT Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Anti-apoptotic protein; overexpression causes G2/M
 CC arrest.
 CC -1- SIMILARITY: BELONGS TO THE SPIN / STSY FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF356353; AAC37566.1; -.
 DR EMBL; BC000044; AAH00044.1; -.
 DR InterPro; IPR003671; Spin_Sety.
 KW Pfam; PF02513; Spin-Sety; 3.
 KW Apoptosis.
 SO SEQUENCE 258 AA; 29158 MW; CAD74289970B4BCD CRC64;
 Query Match
 Best Local Similarity 0.5%; Score 7; DB 1; Length 258;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 549 LDDYKE 555
 DB 177 LDDYKE 183

RESULT 45
 MOB2_YEAST
 ID SPN2_YEAST STANDARD; PRT; 259 AA.
 AC P43563;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Maintenance of ploidy protein MOB2 (Wp1 binder 2).
 GN MOB2 OR YPL035C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 NCBI_TaxID=4932;
 RX MEDLINE=52880; /AB572;
 RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
 RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
 RA Yamayaki M., Tashiro H., Eki T.,
 RT Analysis of the nucleotide sequence of chromosome VI from
 RT Saccharomyces cerevisiae.
 Nat. Genet. 10:261-268(1995).
 CC -1- SIMILARITY: BELONGS TO THE MOB1/PHOCEIN FAMILY.
 CC -----
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 CC -----

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DR EMBL; D50617; BAA09204.1; -
DR PIR; S58648; S58648.
DR SGD; S0001859; MOB2.
DR GO; GO:0005935; C:bud neck; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0003025; F:protein kinase activator activity; IDA.
DR GO; GO:0030012; F:establishment and/or maintenance of cell po. ; IMP.
DR GO; GO:0007096; P:exit from mitosis; IMP.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR InterPro; IPR005301; Mobl.phocein.
DR Pfam; PF03637; Mobl.phocein; 1.
DR SEQUENCE 259 AA; 30112 MW; FDM5D953AFCE282 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 673 RLSTLRNK 679
Db 14 RLSTLRNK 20

RESULT 47
CCG6_HUMAN STANDARD; PRT; 260 AA.
AC Q9BXT2;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Voltage-dependent calcium channel gamma-6 subunit (Neuronal voltage-
gated calcium channel gamma-6 subunit).
GN CACNG6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21100909; PubMed=11170751;
RA Burgess D.L., Gefrides L.A., Foreman P.J., Noebels J.L.;
" A cluster of three novel Ca(2+) channel gamma subunit genes on
chromosome 19q13.4: evolution and expression profile of the gamma
subunit gene family."
RL Genomics 71:339-350(2001).
RN RP
RP SEQUENCE FROM N.A.
RX MEDLINE=21601102; PubMed=11738816;
RA Chu P.-J., Robertson H.M., Best P.M.;
"Calcium channel gamma subunits provide insights into the evolution of
this gene family."
RL Gene 280:37-48(2001).
RT RT
RT "Calcium channel gamma subunits provide insights into the evolution of
this gene family."
CC -1- FUNCTION: THOUGHT TO STABILIZE THE CALCIUM CHANNEL IN AN
INACTIVATED (CLOSED) STATE (BY SIMILARITY).
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FIVE SUBUNITS:
ALPHA-1, ALPHA-2/DELTA, BETA AND GAMMA.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE FMP-22 / EMP / MP20 FAMILY. CACNG
SUBFAMILY.
CC -----
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DR GO; GO:0006816; P:calcium ion transport; NAS.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel.
FT TRANSMEM 43 63 POTENTIAL.
FT TRANSMEM 143 163 POTENTIAL.
FT TRANSMEM 169 189 POTENTIAL.
FT TRANSMEM 221 241 POTENTIAL.
SQ SEQUENCE 260 AA; 28129 MW; 674433E331FDP974 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1072 LLLTLPS 1078
Db 239 LLLTLPS 245

RESULT 48
CCG6_MOUSE STANDARD; PRT; 260 AA.
AC Q8VHM3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Voltage-dependent calcium channel gamma-6 subunit (Neuronal voltage-
gated calcium channel gamma-6 subunit).
GN CACNG6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=BAB/c;
RX MEDLINE=21601102; PubMed=11738816;
RA Chu P.-J., Robertson H.M., Best P.M.;
"Calcium channel gamma subunits provide insights into the evolution of
this gene family."
RL Gene 280:37-48(2001).
RT RT
RT "Calcium channel gamma subunits provide insights into the evolution of
this gene family."
CC -1- FUNCTION: THOUGHT TO STABILIZE THE CALCIUM CHANNEL IN AN
INACTIVATED (CLOSED) STATE (BY SIMILARITY).
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FIVE SUBUNITS:
ALPHA-1, ALPHA-2/DELTA, BETA AND GAMMA.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- TISSUE SPECIFICITY: Highly expressed in muscle.
CC -1- SIMILARITY: BELONGS TO THE FMP-22 / EMP / MP20 FAMILY. CACNG
SUBFAMILY.
CC -----
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239 TTTT 66 6.1.1

RESULT 49

CCG6_RAT

CCG6
08VH

DT 28-F1

RU Mol. Microbiol. 23:799-812(1997).
 CC -1- CATALYTIC ACTIVITY: Shikimate + NADP(+) = 5-dehydroshikimate +
 CC NADPH.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC fourth step.
 CC -1- SIMILARITY: Belongs to the shikimate dehydrogenase family.
 CC -----
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 CC -----
 CC EMBL: U82848; AAC44919.1; -.
 CC HAMAP: MF_00222; -1.
 CC InterPro: IPR006152; Shikimate.
 CC InterPro: IPR006151; Shikimate_DH.
 CC Pfam: PF01488; Shikimate_DH; 1.
 CC TIGRFAMs: TIGR00507; aroG; 1.
 CC DR Aromatic amino acid biosynthesis; Oxidoreductase; NADP-
 CC KW SEQUENCE 269 AA; 28628 MW; 090E539F2B5957F CRC64;
 CC SQ
 CC
 CC Query Match 0.5%; Score 7; DB 1; Length 269;
 CC Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Oy 474 SGTVLL 480
 CC |||||
 CC Db 122 SGTVLL 128
 CC
 CC RESULT 52
 CC Y0AC_LACLA STANDARD; PRT; 281 AA.
 CC ID Y0AC_LACLA
 CC AC 09CFB9;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
 CC DE Hypothetical UPF0230 protein y0ac.
 CC Y0AC OR L11562.
 CC OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 CC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 CC NCBI_TaxID=1360;
 CC [1]
 CC RN SEQUENCE FROM N.A.
 CC RC STRAIN=IL1403;
 CC RA MEDLINE=21235186; Pubmed=11337471;
 CC RA Bojotin A., Winker P., Mauger S., Jallion O., Malarme K.,
 CC RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 CC RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 CC RT lactis ssp. lactis IL1403."
 CC RT Genome Res. 11:731-753(2001).
 CC -1- SIMILARITY: BELONGS TO THE UPF0230 (DRGV) FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE006387; AA05660.1; -.
 CC PIR: B86820; B86820.
 CC InterPro: IPR003797; DegV.
 CC Pfam: PF02645; DUF194; 1.
 CC DR Hypothetical protein; Complete proteome.
 CC KW SEQUENCE 281 AA; 31816 MW; 370A993314FDCP59 CRC64;
 CC SQ
 CC
 CC Query Match 0.5%; Score 7; DB 1; Length 281;
 CC Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 711 DLAEAGV 717
 |||||
 Db 132 DLAEAGV 138
 RESULT 53
 MRP_CLOPE STANDARD; PRT; 284 AA.
 ID MRP_CLOPE
 AC P53381;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE MRP protein homolog.
 GN MRP OR CP2512.
 OS Clostridium perfringens.
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 CC Clostridium.
 CC NCBI_TaxID=1502;
 CC [1]
 CC RN SEQUENCE FROM N.A.
 CC RC STRAIN=13 / Type A;
 CC RX MEDLINE=21664373; Pubmed=11792842;
 CC RA Shimizu T., Ohtani K., Hirakawa H., Onohima K., Yamashita A.,
 CC RA Shiba T., Ogasawara N., Hatori M., Kuhara S., Hayashi H.;
 CC RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 CC RT flesh-eater."
 CC RT Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 CC [2]
 CC RN SEQUENCE OF 50-189 FROM N.A.
 CC RC STRAIN=CPN50;
 CC RX MEDLINE=96032407; Pubmed=7559358;
 CC RA Katayama S.-I., Dupuy B., Garnier T., Cole S.T.;
 CC RT "Rapid expansion of the physical and genetic map of the chromosome of
 CC RT Clostridium perfringens CPN50."
 CC RT J. Bacteriol. 177:5680-5685(1995).
 CC -1- FUNCTION: NOT KNOWN.
 CC -1- SIMILARITY: BELONGS TO THE MRP/NBP35 FAMILY OF ATP-BINDING
 CC PROTEINS.
 CC -----
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 CC -----
 CC EMBL: AP003194; BA82218.1; -.
 CC DR EMBL: X86509; CA60227.1; -.
 CC DR InterPro: IPR000808; MRP family.
 CC DR PROSITE: PS01215; MRP; 1.
 CC ATP-binding; Complete proteome.
 CC FT NP BIND 46
 CC SEQUENCE 284 AA; 30835 MW; 8CB32F8BF0510EAF CRC64;
 CC SQ
 CC
 CC Query Match 0.5%; Score 7; DB 1; Length 284;
 CC Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Oy 229 SKKSEE 235
 CC |||||
 CC Db 232 SKKSEE 238
 CC
 CC RESULT 54
 CC ID1_NPVAC STANDARD; PRT; 286 AA.
 CC ID1_NPVAC
 CC AC P41435;
 CC DT 01-NOV-1995 (Rel. 32, Created)
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Apoptosis inhibitor 1 (IAP-1).
GN IAP1.
OS Autographa californica nuclear polyhedrosis virus (AcNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
OC Nucleopolydnaviruses.
OX NCBI_TaxID=46015;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6;
RX MEDLINE=94303173; PubMed=8030224;
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.,
RT "The complete DNA sequence of Autographa californica nuclear
RT polyhedrosis virus."
RL Virology 202:586-605(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=E2;
RX MEDLINE=93079853; PubMed=133113;
RA Braunagel S.C., Daniel K.D., Reilly L.M., Guarino L.A., Hong T.,
RT Sumners M.D.;
RT Sequence, genomic organization of the EcoRI-A fragment of Autographa
RT californica nuclear polyhedrosis virus, and identification of a
RT viral-encoded protein resembling the outer capsid protein VP8 of
RT rotavirus."
RL Virology 191:1003-1008(1992).
CC -1- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY
CC PREVENTING VIRAL STIMULATION OF APOPTOSIS.
CC -1- SIMILARITY: Contains 2 BIR repeats.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
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CC -----
DR EMBL: L2858; AA6657.1; -;
DR EMBL: M9361; AA66796.1; -;
DR PIR: D36828; D36828.
DR HSSP: Q13490; 108H.
DR InterPro: IPR001841; Znf_xing.
DR Pfam: PF00653; BIR_2.
DR SMART: SM00228; BIR_2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
DR PROSITE: PS50089; ZF_RING_1; PALSR_NEG.
DR KX Apoptosis; zinc-finger; Repeat.
FT REPEAT 29
FT REPEAT 131
FT ZN_FING 238
FT ZN_FING 274
SQ SEQUENCE 286 AA; 33320 MW; FFE505A3SEFLBEA CRC64;
Query Match 0.5%; Score 7; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE zinc finger protein 75.
GN ZNF75.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue: lung fibroblast;
RX MEDLINE=9416987; PubMed=828823;
RA Villa A., Zucchi I., Pila G., Strina D., Susani L., Morali F.,
RA Patrosso C., Fratini A., Lucchini F., Repetto M., Sacco M.G.,
RT "ZNF75: isolation of a cDNA clone of the KRAB zinc finger gene
RT subfamily mapped in YACs 1 Mb telomeric of HPR1."
RL Genomics 18:223-229(1993).
RN [2]
RP SEQUENCE OF 139-289 FROM N.A.
RA Marino M., Archidaco N., Franze N., Rosati M., Rocchi M.,
RA Balabio A., Grimaldi G.,
RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION MAY BE INVOLVED IN TRANSCRIPTIONAL REGULATION.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potentially).
CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.
CC -1- SIMILARITY: Contains 1 KRAB domain.
CC -1- SIMILARITY: Contains 5 C2H2-type zinc fingers.
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CC -----
DR EMBL: S67970; AA829696.1; -;
DR EMBL: X69010; CA48147.1; -;
DR PIR: A48913; A48913.
DR HSSP: P25490; 12NM.
DR Genem: HGNC:13145; ZNF75.
DR MIM: 314977; -;
DR GO: GO:0005634; C:nucleus; NAS.
DR GO: GO:0003677; F:DNA binding activity; NAS.
DR GO: GO:0008270; F:zinc ion binding activity; NAS.
DR GO: GO:0006355; P:regulation of transcription activity; NAS.
DR InterPro: IPR001909; KRAB.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF01352; KRAB_1.
DR Pfam: PF00096; ZF_C2H2; 5.
DR PRINTS: PR00044; ZINC_FINGER.
DR PRODOM: PD000003; ZNF_C2H2; 3.
DR SMART: SM00353; KRAB_1.
DR SMART: SM00353; ZNF_C2H2; 5.
DR PROSITE: PS50805; KRAB; 1.
DR PROSITE: PS50028; ZINC_FINGER_C2H2_1; 5.
DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 5.
DR KX Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
FT DOMAIN 14
FT ZN_FING 144
FT ZN_FING 172
FT ZN_FING 200
FT ZN_FING 228
FT ZN_FING 256
SQ SEQUENCE 289 AA; 33683 MW; 9657B00B1DF64DE CRC64;
Query Match 0.5%; Score 7; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      |||||
        8 PESTSUL 14

RESULT 56
METP_BUCAP STANDARD; PRT; 292 AA.
AC 08KA62:
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 5,10-methyleneletrahydrofolate reductase (EC 1.7.99.5).
MEFP OR BUSG043.
GN Buchnera aphidicola (subsp. Schizaphis graminum).
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
CC NCBI_TaxID=98794;
CX [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22084549; PubMed=12089438;
RA Tamas I., Klassen L., Canhaeck B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
RT "50 million years of genomic stasis in endosymbiotic bacteria.";
RL Science 296:2376-2379(2002)
CC -1- CRYSTALLIC ACTIVITY: 5-methyltetrahydrofolate + acceptor = 5,10-
CC -1- methylenetetrahydrofolate + reduced acceptor.
CC -1- COPACTOR: FAD (By similarity).
CC -1- PATHWAY: Methionine biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE METHYLENETETRAHYDROFOLATE REDUCTASE
CC (EC 1.5.1.20/EC 1.7.99.5) FAMILY.
CC -----
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CC -----
CC EMBL: AEO14080; AAM6764.1; -.
CC InterPro: IPR004620; Fadh2_bact.
CC InterPro: IPR003171; Methylotf_redctase.
CC DR Pfam: PF02219; MTHFR, 1.
CC DR TIGRPFAMs: TIGR00676; fadh2; 1.
CC KW Oxidoreductase; Flavoprotein; FAD; Methionine biosynthesis;
CC Complete proteome.
CC SQ SEQUENCE 292 AA; 33676 MW; 0660895E1B065E71 CRC64;

Query Match 0.5%; Score 7; DB 1; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 478 VLKKIA 484
Db 137 VLKKIA 143

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RX MEDLINE=93273699; PubMed=8501037;
RA Apelian D., Inouye S.; factor of Myxococcus xanthus.";
RT "A new putative sigma factor of Myxococcus xanthus.";
RL J. Bacteriol. 175:3335-3342(1993).
CC -1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
CC ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
CC THEN IS RELEASED. THIS SIGMA FACTOR IS ESSENTIAL FOR NORMAL
CC FRUITING BODY FORMATION.
CC -1- SIMILARITY: Belongs to the sigma-70 factor family.
CC -----
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CC -----
CC EMBL: L12892; AAA25408.1; -.
CC PIR: A40587; A40587.
CC DR HSSP: P00579; 1SIG.
CC DR InterPro: IPR000943; Sigma_70.
CC DR Pfam: PF00140; sigma70_r1_2; 1.
CC DR Pfam: PF04542; sigma70_r2_1.
CC DR Pfam: PF04538; sigma70_r3_1.
CC DR Pfam: PF04545; sigma70_r4_1.
CC DR PRINTS: PR00046; SIGMA70RECT.
CC DR PROSITE: PS00715; SIGMA70_1; FALSE NEG.
CC DR PROSITE: PS00716; SIGMA70_2; FALSE NEG.
CC KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
CC DNA-binding.
CC FT DOMAIN 73 86 POLYMERASE CORE BINDING (POTENTIAL).
CC FT DNA_BIND 250 269 H-T-H MOTIF (BY SIMILARITY).
CC SQ SEQUENCE 295 AA; 33433 MW; DB2D4E7B3C7FA49 CRC64;

Query Match 0.5%; Score 7; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 713 ABAQVDE 719
Db 284 ABAQVDE 280

RESULT 58
Y326 MYCGB STANDARD; PRT; 295 AA.
AC P47568:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0230 protein MG326.
GN MG326.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
CC NCBI_TaxID=2097;
CX [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-P., Dougherty B.A., Bort K.F., Hu P.-C., Butler T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
CC -1- SIMILARITY: BELONGS TO THE UPF0230 (DEGV) FAMILY.
CC -----
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DR EMBL: U39714; AACV1550.1; -
DR PIR: A64236; A64236.
DR TIGR: MG326; -
DR InterPro: IPR003797; DegV.
DR Pfam: PF02645; DUF194; 1.
DR TIGRFAMs: TIGR00762; DegV; 1.
DR Hypothetical protein: Complete proteome.
SQ SEQUENCE 295 AA; 33413 MW; 04610881C0F841EE CRC64;

Query Match Best Local Similarity 100.0%; Score 7; DB 1; Length 295;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 VOLAKEL 38
Db 102 VOLAKEL 108

RESULT 59
ID NIFD_NOSCO STANDARD; PRT; 296 AA.
AC P52337;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1996 (Rel. 38, Last annotation update)
DE Nitrogenase molybdenum-iron protein alpha chain (EC 1.18.6.1)
GN (Nitrogenase component I) (Dinitrogenase) (Fragment).
OS Nostoc commune.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
RX NCBI_Taxid=1178;

RP SEQUENCE FROM N.A.
RC STRAIN=UTEX 584;
RA MEDLINE=94341563; PubMed=80631099;
RA Angeloni S.V., Poter M.,
RT Analysis of the sequences within and flanking the
RT cyanoglobin-encoding gene, glnB, of the cyanobacterium Nostoc commune
RT UTEX 584.";
RL Gene 146:133-134(1994).

CC -1- FUNCTION: THE KEY ENZYMAIC REACTIONS IN NITROGEN FIXATION ARE
CC CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
CC IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN
CC -1- CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATP
CC -1- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS THAT BINDS
CC 30-32 FE, 2 MO, AND INORGANIC SULFUR.
CC -1- SIMILARITY: BELONGS TO THE NIFD/NITF/NIFE/NIFN FAMILY.

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DR EMBL: L23514; AAA21839.1; -
DR HSRP: P07328; 3MTN.
DR InterPro: IPR000318; Nitrogenase comp1.
DR Pfam: PF00148; Oxidized nitro; 1.
DR PROSITE: PS00090; Nitrogenase 1_2; 1.
DR PROSITE: PS00699; Nitrogenase 1_1; 1.
KM Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.
FT NON TER 296
SQ SEQUENCE 296 AA; 32987 MW; 38061E678E8FD382 CRC64;

Query Match Best Local Similarity 100.0%; Score 7; DB 1; Length 296;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1146 KLVRLIQ 1152
Db 132 KLVRLIQ 138

RESULT 60
ID BIR7_HUMAN

AC O96CA5; O96QV0; Q9H2A8; Q9HAP7; STANDARD; PRT; 298 AA.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 7 (Kidney inhibitor of
DE apoptosis protein) (KIAP) (Melanoma inhibitor of apoptosis protein)
DE (ML-IAP) (LIVIN).
GN BIRC7 OR KIAP OR ML-IAP OR LIVIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
RX NCBI_Taxid=9606;

RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fetal kidney;
RA MEDLINE=21092523; PubMed=11162435;
RA Lin J.-H., Deng G., Huang Q., Morner J.,
RT "KIAP, a novel member of the inhibitor of apoptosis protein family,"
RL Biochem. Biophys. Res. Commun. 279:820-831(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Melanoma;
RA MEDLINE=21223043; PubMed=11322947;
RA Ashhab Y., Alian A., Pollack A., Panet A., Yehuda D.B.,
RT "Two splicing variants of a new inhibitor of apoptosis gene with
RT different biological properties and tissue distribution pattern,"
RL FEBS Lett. 495:56-60(2001).
RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Kidney;
RA PubMed=11024045;
RA Kasot G.M., Gomes B.C.,
RT "LIVIN, a novel inhibitor of apoptosis protein family member,"
RL J. Biol. Chem. 276:3238-3246(2001).
RN [4]

RP SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).
RA MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Aghvost J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrakas G., Almeida J.P., Babbage A.X., Baggeley C.L.,
RA Beasley O.P., Barlow K.F., Bates K.N., Beard L.M., Beare D.H.,
RA Buck D., Burdill M.D., Butler A.P., Bridgeman A.M., Brown A.J.,
RA Chapman J.C., Clamp M., Clark G., Carder C., Carter N.P.,
RA Clegg S., Cobley V.E., Collier R.E., Connor B.E., Corby N.R.,
RA Coulson A.G., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington D.V., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafton A.G., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.B.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Kay M.P., Kimberley A.M., King A., Klesch K., Johnson C.M., Johnson D.,
RA Lhveestialho M.H., Levertha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Milne S.A., Mistry D., McCormack L.J., McElroy D.M., Murray A.A.,
RA Oliver K., Parker A., Pearce M.J.F., Mullikin J.C., Nicolson T.,
RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showken R.,
RA Skuce C.D., Smith N.L., Soderlund C., Steward C.A., Sutton J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin R., Wall M., Wallis S.A.,
RA Whitehead S.V., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,


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RESULT 61
GLXB_RHIME STANDARD; PRT; 300 AA.
ID GLXB_RHIME
AC 087390;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GLXB OR R00087 OR SMC02610.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OX NCBI_TaxId=382;
RN [1]_TaxId=382;
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RA Powers E.L., Vuyyuru V., Kahn M.L.;
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RA MEDLINE=21396507; PubMed=1168130;
RA Capela D., Barloy-Hubier F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Bostard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godle T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramberger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021."
RL Proc Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -1- SIMILARITY: Contains 1 type-2-glutamine amidotransferase domain.
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CC
CC EMBL; AF055583; AAC62220.1; ALT INIT.
DR EMBL; AL51782; CAC41474.1; ALT INIT.
DR InterPro; IPR000583; GATase_2.
DR Pfam; PF00310; GATase_2; 1.
DR PROSITE; PS00443; GATASE TYPE II; 1.
KW Transferase; Glutamine amidotransferase; Complete proteome.
FT INIT_MDT 0 BY SIMILARITY.
FT ACT_SITE 1 1 GATASE (BY SIMILARITY).
SQ SEQUENCE 300 AA; 31987 MW; 98596E4A89509248 CRC64;
Query Match 0.5%; Score 7; DB 1; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 711 DLAEAGV 717
Db 68 DLAEAGV 74

RESULT 62
HEMK_MYCTU STANDARD; PRT; 304 AA.
ID HEMK_MYCTU
AC Q10602;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hemk protein homolog (EC 2.1.1.-) (M.MuHemkP).
GN HEMK OR RV1300 OR MT133 OR MTCY373.20.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RA MEDLINE=98295987; PubMed=96344230;
RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gae S., Barry C.E. III, Tekala F.,
RA Davies K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Horsley T., Devlin K., Felwell T., Gentles S., Harlin N., Holroyd S.,
RA Holmes S., Osborne J., Krogan A., McLean J., Moule S., Murphy L.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares J.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fieschmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE HEMK FAMILY.
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CC
CC EMBL; Z73419; CAA97733.1; ALT INIT.
DR EMBL; AF070008; AKK45601.1;
DR REBASE; 4465; M.MuHemkP.
DR TIGR; MT1339;
DR TubercuList; RV1300;
DR InterPro; IPR004556; Hemk.
DR InterPro; IPR002052; NE Mcase.
DR TIGRPM6; TIGR00051; SAM bind.
DR PROSITE; PS00092; NE MTASE; UNKNOWN.1.
KW Transferase; Methyltransferase; Complete proteome.
FT CONFLICT 173 173 C (IN REF. 2).
SQ SEQUENCE 304 AA; 32459 MW; 65CFA7F02EA3455 CRC64;
Query Match 0.5%; Score 7; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 712 LAEAGVD 718
Db 14 LAEAGVD 20

RESULT 63
BEL1_SFV1 STANDARD; PRT; 308 AA.
ID BEL1_SFV1
AC P29169;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE BEL-1 protein.
GN BEL-1 OR TAF.
OS Simian foamy virus (type 1) (SFV-1).
OC Viruses; Retrovirdae; Retroviridae; Spumavirus.
OX NCBI_TaxId=11964;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RA MEDLINE=98295987; PubMed=96344230;
RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gae S., Barry C.E. III, Tekala F.,
RA Davies K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Horsley T., Devlin K., Felwell T., Gentles S., Harlin N., Holroyd S.,
RA Holmes S., Osborne J., Krogan A., McLean J., Moule S., Murphy L.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares J.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fieschmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE HEMK FAMILY.
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CC
CC EMBL; Z73419; CAA97733.1; ALT INIT.
DR EMBL; AF070008; AKK45601.1;
DR REBASE; 4465; M.MuHemkP.
DR TIGR; MT1339;
DR TubercuList; RV1300;
DR InterPro; IPR004556; Hemk.
DR InterPro; IPR002052; NE Mcase.
DR TIGRPM6; TIGR00051; SAM bind.
DR PROSITE; PS00092; NE MTASE; UNKNOWN.1.
KW Transferase; Methyltransferase; Complete proteome.
FT CONFLICT 173 173 C (IN REF. 2).
SQ SEQUENCE 304 AA; 32459 MW; 65CFA7F02EA3455 CRC64;
Query Match 0.5%; Score 7; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 712 LAEAGVD 718
Db 14 LAEAGVD 20

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RP SEQUENCE FROM N.A.
RX MEDLINE=91276270; PubMed=1647358;
RA Kupiec J.-J., Kay A., Hayat M., Ravier R., Peries J., Gilbert F.;
RT "Sequence analysis of the simian foamy virus type 1 genome.";
RL Gene 101:185-194(1991).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=91237804; PubMed=1851862;
RA Meria A., Shaw K.E., Pratt-Lowe E., Barry P.A., Lindw P.A.;
RT "Identification of the simian foamy virus transcriptional
transactivator gene (tafv).";
RL J. Virol. 65:12903-12909(1991).
CC -1- FUNCTION: THIS PROTEIN IS A TRANSCRIPTIONAL TRANSACTIVATOR.
CC
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RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96044033; PubMed=9384377;
RA Kunst F., Ogawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Berteiro M.G., Beesleres P., Bolotin A., Borczyk S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano N.J., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Dentzer P., Devine K.M., Dusterhoff A., Ehrlich S.D., Emerson P.T.,
RA Enlian K.D., Ertugron U., Fabre C., Ferrati B., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Gallier N.,
RA Ghim S.Y., Glaser P., Goffeau A., Goldlighty E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haeck J., Harwood C.R., Henaut A.,
RA Hilbert R., Holzapfel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasehara Y., Klier-Bianchini M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Maeda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Preece E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche M., Rose M., Sadate Y.,
RA Sato T., Scanlan B., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemura K.,
RA Takouchi M., Tamakoshi A., Tanaka T., Terpestra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vasarotti A.,
RA Viari A., Wandt R., Wedler E., Wedler H., Weitzegger T.,
RA Winters P., Wipat A., Yamamoto K., Yamane K., Yasunoro K., Yata K.,
RA Yoshida K., Yoshikawa H.P., Zumbstein E., Yoshikawa H., Zumbstein
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256(1997).
RN [4]
RP FUNCTION.
RX MEDLINE=94321341; PubMed=8045899;
RA Jin S., Sonenshein A.L.;
RT "Transcriptional regulation of Bacillus subtilis citrate synthase
genes.";
RL J. Bacteriol. 176:4680-4690(1994).
CC -1- FUNCTION: NEGATIVE REGULATORY PROTEIN FOR THE CITR GENE FOR
CITRATE SYNTHASE I.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
CC
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OY 107 AGLTRLP 113
DB 266 AGLTRLP 272

RESULT 65

GLSA_RHIME STANDARD: PRT: 315 AA.
ID_GLSA_RHIME

AC 092PH0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB Glutaminase (EC 3.5.1.2).
GN GLSA OR R01786 OR SMC00486.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OX Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
RN NCBI_TaxId382;

SEQUENCE FROM N.A.

RA STRAIN=1021;
RA MEDLINE=21396507; PubMed=1181430;
RA Capela D., Barloy-Hubler F., Guzy J., Bothe G., Ampe F., Batut J.,
RA Godtard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S.,
RA Godtard T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,
RA Pohl T., Portetale D., Fuenler A., Purnelle B., Rampeger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.,
RA Sinorhizobium meliloti strain 1021.
RT Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
RL -1- CANDALYTIC ACTIVITY: L-glutamate + H(2)O = L-glutamate + NH(3).
CC -1- SIMILARITY: BELONGS TO THE GLUTAMINASE FAMILY.

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DR EMBL: A1591786; CAC63655.1;
DR HAMAB: MF 00313;
DR InterPro: IPR007043; Glutaminase.
DR Pfam: PF04960; Glutaminase; 1.
DR Hydrolase; Complete proteome.
SQ SEQUENCE 315 AA; 33991 MW; CB3A52CAB20A2B64 CRC64;

Query Match 0.5%; Score 7; DB 1; Length 315;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 299 LARAGUF 305
DB 210 LARAGUF 216

RESULT 66

RFC4_YEAST STANDARD: PRT: 323 AA.
ID_RFC4_YEAST

AC PA035;
DT 01-PRB-1995 (Rel. 31, Created)
DT 01-PRB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Activator 1 37 kDa subunit (Replication factor C subunit 4)
DR Replication factor C4.
GN RFC4 OR YOL094C OR O0923.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxId=4932;

SEQUENCE FROM N.A.

RA STRAIN=W303;
RA MEDLINE=94342386; PubMed=8063832;
RA Li X., Burgers P.M.J.;
RT "Cloning and characterization of the essential Saccharomyces
RT cerevisiae RFC4 gene encoding the 37-kDa subunit of replication
RT factor C.";
RL J. Biol. Chem. 269:21880-21884(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=8288C;
RX MEDLINE=85379808; PubMed=7651383;
RA Cullmann G., Fien K., Kobayashi R., Stillman B.,
RT Characterization of the five replication factor C genes of
RT Saccharomyces cerevisiae.";
RL Mol. Cell. Biol. 15:4661-4671(1995).
RN [3]

SEQUENCE FROM N.A.

RA STRAIN=8288C / FY1679;
RA MEDLINE=96021609; PubMed=8533473;
RA Zumestein E., Pearson B.M., Kallogeropoulos A., Schweizer M.,
RA "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RA more than twice as many unknown as known open reading frames.";
RL Yeast 11:975-986(1995).
RN [4]

SEQUENCE FROM N.A.

RA Pubmed=9169874;
RA Dujon B., Albermann K., Aldea M., Alexandraki D., Ansgore W.,
RA Arino J., Benes V., Bohn C., Bolotin-Fukuhara M., Bordonne R.,
RA Boyer J., Canasas A., Casamayor A., Caste C., Chet G.,
RA Czapluch C., Dalgman-Fornier B., Dang D.V., de Haan M., Delieu H.,
RA Durand P., Fairhead C., Feldmann H., Gallon L., Gailson F.,
RA Gano F.-U., Gancedo C., Goffeau A., Goulding S.E., Givelli L.A.,
RA Habibi B., Hand N.J., Hani J., Hattendorf U., Hebling U.,
RA Hernandez Y., Herrero E., Heumann K., Hiesel R., Hliger F., Hofmann B.,
RA Hollenberg C.P., Hughes B., Jentiaux J.-C., Kallogeropoulos A.,
RA Katsoulou C., Korides E., Lafuente M.J., Landt O., Louis E.J.,
RA Maere C., Madania A., Manhaupt G., Marck C., Martin R.P.,
RA Mees H.-W., Michaux A., Manhaupt G., Marck C., Martin R.P.,
RA Perrin A., Petersson B., Poch O., Pohl T.M., Polley R.,
RA Portetale D., Pujol A., Purnelle B., Ramezani Rad M., Rechmann S.,
RA Schweiger C., Schweizer M., Sor F., Steyer F., Tarasov I.A.,
RA Todorou C., Tellein H., Thierry A., Tobiasch E., Tzermia M.,
RA Uhlen M., Unselid M., Valens M., Vandenbol M., Vetter H., Vieck C.,
RA Voet M., Volckaert G., Voss H., Wambutt R., Weidner S., Wiemann S.,
RA Winkler B., Wolfe K.H., Zollner A., Zumestein E., Kline K.,
RT The nucleotide sequence of Saccharomyces cerevisiae chromosome XV.";
RL Nature 387:98-102(1997).

FUNCTION: The elongation of primed DNA templates by DNA polymerase

CC delta and epsilon regions requires the action of the accessory proteins
CC -1- SUBUNIT: Heteropentamer of subunits RFC1, RFC2, RFC3, RFC4 and
CC RFC5 that forms a complex with PCNA in the presence of ATP. RFC4
CC forms a tight complex with RFC3.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: BELONGS TO THE ACTIVATOR 1 36 TO 40 kDa SUBUNITS
CC FAMILY.

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DR EMBL: L20502; AAA34970.1;
DR EMBL: U26030; AAC49653.1;
DR EMBL: X63121; CAA58185.1;
DR EMBL: Z74836; CAA99106.1;
DR PIR: A53845; A53845.
DR SGD: S0005454; RFC4.

GO: GO:0005663; C:DNA replication factor C complex; IDA.

DR GO: GO:0006272; P:leading strand elongation; IDA.
 DR GO: GO:0007062; P:sister chromatid cohesion; IPI.
 DR InterPro: IPR003593; AAA_Atpase.
 DR InterPro: IPR003593; AAA_Atpase_central.
 DR InterPro: IPR000862; RFDomain.
 DR Pfam: PF00004; AAA: 1.
 DR SMART: SM00382; AAA: 1.
 DR DNA replication; ATP-binding; Nuclear protein; DNA-binding.
 DR NP_BIND 56
 GO BIND 323 AA; 36149 MW; 1F5F35F071331P CRC64;
 GO SEQUENCE

Query Match
 Best local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

374 SNLEDS1 380
 243 SNLEDS1 249

RESULT 67
 DAPF_LISMO STANDARD; PRT; 329 AA.
 AC 08Y5N9;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Diaminopimelate epimerase (EC 5.1.1.7) (DAP epimerase).
 GN DAPF OR LMO2018.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 CX NCBI_TaxID=1639;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC STRAIN=EGD-e / Serovar 1/2a;
 RX MEDLINE=21537279; PubMed=1167669;
 RA Glaser P., Frangeul L., Buchliesser C., Rusniok C., Amend A.,
 Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 Charbit A., Cherouani F., Couve E., de Lencastre A., Deboux P.,
 Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 Gautier L., Geisel W., Garcia-del Portillo F., Garrido P.,
 Gantier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunz F., Kurapkut G.,
 Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,
 Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 Remmel B., Rose M., Schluter T., Simoes N., Tietz A.,
 Vazquez-Boland J.-A., Voas H., Weiland J., Cosset P.;
 "Comparative genomics of Listeria species";
 Science 294:849-853(2001).
 RL Science 294:849-853(2001).
 CC -1- CATALYTIC ACTIVITY: Lysine + 2,6-diaminoheptanedioate = meso-
 diaminoheptanedioate.
 CC -1- PATHWAY: Biosynthesis of lysine from aspartate semialdehyde; sixth
 step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the diaminopimelate epimerase family.
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EMBL: AL591981; CAD00096.1; -.
 PIR: A81327; A81327.
 LIEB: LMO02018; -.
 HAMAP: MF_00197; -; 1.
 DR InterPro: IPR001653; DAP epimerase.
 DR Pfam: PF01678; DAP epimerase; 2.
 DR PROSITE: PS01326; DAP EPIMERASE; 1.
 KW Isomerase; lysine biosynthesis; Complete proteome.
 FT ACT_SITE 82 82 BY SIMILARITY.

FT ACT_SITE 233 233 BY SIMILARITY.
 SQ SEQUENCE 329 AA; 36070 MW; 9B592BFFA8A83CD CRC64;
 GO SEQUENCE

Query Match
 Best local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

760 LQSDROE 766
 182 LQSDROE 188

RESULT 68
 XDHA_BACSU STANDARD; PRT; 330 AA.
 ID XDHA_BACSU
 AC 03147;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable xanthine dehydrogenase subunit A (EC 1.1.1.204) (XDase
 subunit A).
 GN PUCA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=1423;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunz P., Ogassawara N., Moszer I., Albertini A.M., Alloni G.,
 Azevedo V., Besterio M.G., Besieres P., Bolotin A., Borchert S.,
 Borrias R., Bourcier L., Brans A., Braum M., Brignell S.C., Bron S.,
 Brouillet S., Bruesch C.V., Caldwell B., Capuano V., Carter N.M.,
 Choi S.K., Codani J.J., Conneron I.F., Cummings S.D., Daniel R.A.,
 Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.J., Emmerson P.T.,
 Entian K.D., Errington J., Fabret C., Ferrari B., Foulger D.,
 Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
 Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 Hilbert H., Holsappel S., Hosono S., Hulo M.F., Itaya M., Jones L.,
 Joris B., Karamata D., Kasehara Y., Klaerner-Blaichard M., Klein C.,
 Kobayashi Y., Koester P., Koningsleyn G., Krogh S., Kumano M.,
 Kunita K., Lapidus A., Lardinois S., Laber J., Lazarevic V.,
 Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue V.,
 Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 Noone D., O'Reilly M., Ogawa K., Ogilwara A., Oudega B., Park S.H.,
 Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 Pressecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 Rieger M., Rivolta C., Roche E., Roche E., Rose M., Sadie Y.,
 Sato T., Scanlan B., Schleich S., Schroeder K., Scottone F.,
 Setiguchi J., Sekowska A., Seior S.J., Serron P., Shin B.S., Solio B.,
 Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
 Torato V., Uchiyama S., Vandenbol M., Vannier P., Vassart A.,
 Viari A., Wambutt R., Wedler E., Wedler H., Weitzsaecker T.,
 Winters P., Wipat K., Yamamoto H., Yaman K., Yasumoto K., Yata K.,
 Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zanchin A.,
 "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis";
 Nature 390:249-256(1997).
 RL Nature 390:249-256(1997).
 CC FUNCTION.
 RX STRAIN=168;
 MEDLINE=1242727; PubMed=11344136;
 RA Schultz A.C., Nygaard P., Saxild H.H.;
 "Functional analysis of 14 genes that constitute the purine catabolic
 pathway in Bacillus subtilis and evidence for a novel regulon
 controlled by the PucR transcription activator";
 J. Bacteriol. 183:3293-3302(2001).
 CC -1- FUNCTION: Oxidizes hypoxanthine and xanthine to uric acid. PucA
 subunit could exert a molybdenum cofactor recruiting function.
 CC -1- CATALYTIC ACTIVITY: Xanthine + NAD(+) + H(2)O = urate + NMDH.
 CC -1- PATHWAY: Purine catabolism.

Matches	7; Conservative	0; Mismatches	0; Indels	0; Gaps
1100	KPCLCE	1106		
48	KPCLCTP	E4		

08XHP0	STANDARD;	PRT;	337 AA.
28-FEB-2003 (Rel. 41, Created)			
28-FEB-2003 (Rel. 41, Last delivered)			

Clostridium perfringens;
 Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 NCBI TaxId=1502;
 Clostridium perfringens CPE2442 (EC 2.7.3.-).

SEQUENCE FROM N.A.
STRAIN=13 / Type A:
MEDLINE=21664373; PubMed=11792842;
Shimizu m

Shimizu T., Ohtani K., Hirakawa H., Oshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of *Clostridium perfringens*, an anaerobic flesh-eater.";

Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
- - SIMILARITY: BELONGS TO THE ATP:GUANIDINE PHOSPHOTRANSFERASE FAMILY.
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```

EXHL, AP003194; BAb82148, 1; -.
HAMAD, MF_00602; -. 1.
InterPro: IPR000749; ATP_gua_Ptrans.
Pfam: PF00217; ATP_gua_Ptrans; 1.
PROSITE: PS00112; ATP_gua_Ptrans; 1.

```

0.5%, Score 7; DR 1; Length 22
 Hypothetical protein; Transferase; Kinase; Complete proteome.
 SEQUENCE 337 AA: 38765 MM; 4BC7C84BE1FDAD1 CRC64;
 ery Match

[illegible]

200 NKDVANI 205
J. 71
HIMAN

TGDS_HUMAN	STANDARD;	PRT; 350 AA.
094455; Q9H1T9;		
15-SEP-2003 (Rel. 42, Created)		
15-SEP-2003 (Rel. 42, Last Reviewed)		

15-SP-2003 (Rel. 42, Last sequence update)
dUDP-D-glucose 4,6-dehydratase (EC 4.2.1.46).
TCDS.
Homo sapiens (Human).
Eukaryota; Vertebrata; Mammalia; Primates; Hominidae; Homo

Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euhetia; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;

SEQUENCE FROM N.A.
Sturla L., Bisso A., Zanardi P.
Mammalia; *Eutheria*; *Carnivora*; *Felidae*
[1] NCBI TaxID=9606;
Primates; *Catarrhini*; *Hominidae*; *Homo*.
[1]

SEQUENCE FROM N.A.
 CURIA L., BISSO A., ZANARDI D., DE FLORA A., TONETTI M.;
 Identification of dUDP-D-glucose 4,6 dehydratase in human cells.;

RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RP SEQUENCE FROM N.A.
 RA Seppala R., Lehto V.-P., Gahl W.A.;
 RT "Similar to Haemophilus influenzae dTDP-glucose 4,6-dehydratase.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Klei S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dictencko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carinini P., Prange C.,
 RA Rata S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McBean P.J., McKernan K.U., Malek J.A., Gamarate P.H.,
 RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzyzanski M.I., Skalska U., Smallus D.E.,
 RA Scherf A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 106-350 FROM N.A.
 RA Bates K.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: dTDP-glucose = dTDP-4-dehydro-6-deoxy-D-
 CC glucose + H(2)O.
 CC -1- COFACTOR: NAD (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY. DTPD-GLUCOSE
 CC DEHYDRATASE SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; AJ006068; CA006840.1; -
 DR EMBL; AF048686; AAD50061.1; -
 DR EMBL; BC033675; AA033675.1; -
 DR EMBL; AL139318; CAC19462.1; -
 DR HSSP; P27830; 1BXK.
 DR Genew; HGNC:20324; TGD5.
 DR InterPro; IPR001509; Epimerase_Dh.
 DR Pfam; PF01370; Epimerase_1.
 KW Lyase, NAD. 350 AA; 40214 MW; EE427AD1D191EA3D CRC64;
 SQ SEQUENCE

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mannonate dehydratase (EC 4.2.1.8) (D-mannonate hydrolase).
 GN UXA OR CPE0151.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / Type A.
 RX MEDLINE=21664373; PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kohara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 CC -1- CATALYTIC ACTIVITY: D-mannonate = 2-dehydro-3-deoxy-D-glucuronate +
 CC H(2)O.
 CC -1- PATHWAY: Glucuronate pathway.
 CC -1- SIMILARITY: Belongs to the mannonate dehydratase family.
 CC -----
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 CC -----
 DR EMBL; AP003185; BAB79857.1; -
 DR HAMAP; MF_00106; -; 1.
 DR InterPro; IPR004628; Man_dehyd.
 DR Pfam; PF03786; UXA; 1. _dehyd.
 DR TIGSFAM; TIGR00695; uxa; 1.
 KW Lyase; Complete proteome.
 SQ SEQUENCE 350 AA; 40293 MW; 80FB0F9CFFD78A0B CRC64;
 QY Query Match 0.5%; Score 7; DB 1; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 712 LAEGVD 718
 |||||
 93 LAEGVD 99
 RESULT 73
 HTSB_STAM STANDARD; PRT; 352 AA.
 AC Q99V99;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Histidinol-phosphate aminotransferase (EC 2.6.1.9) (imidazole acetyl-
 DE phosphate transaminase).
 GN HISC OR SAV0724 OR SA0679.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878, 158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699, and N315;
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama T., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-O., Ito T.,
 RA Kanamori M., Matsunari H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Ohshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratsuki K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";

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 CC -----

DR EMBL, AF003360: BAB56986.1; --
DR EMBL, AF003361: BAB56987.1; --
DR PIR, E89844: E89844.1; --
DR HAMAP, MF_010733; --, 1.
DR InterPro, IPR004839: AminoTransferase1/2.
DR InterPro, IPR005861: HisE_AminoTrans.
DR InterPro, IPR001917: NHRnaE2.
DR Pfam, PF00135: AminoTran_1_2; 1.
DR TIGRfam, TIGR01141: HisC; 1.
DR PROSITE, PS00599: AA_TRANSFERSER_CLASS_2; 1.
DR HisE_din_biosynthesis: Transferase AminoTransferase;
KW Pyridoxal phosphate; Complete proteome.
FT PYRIDOXAL 221 221
SQ SEQUENCE 352 AA; 39768 MW; DDA6A041524DD700 CRC64;

Query Match	0.5%	Score 7,	DB 1,	Length 352,
Best Local Similarity	100.0%	Fred. No. 1.5e-02;		
Matches	7,	Conservative	0,	Mismatches 0,
				Indels 0,
				Gaps 0.
Qy	103	ILFGAGL	109	
Dp	83	ILFGAGL	89	

RESULT 74	HIS8_STAAW	STANDARD;	PRT;	352 AA.
ID	HIS8_STAAW			
AC	Q8NNX3;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DT	Histidinol-phosphate aminotransferase (EC 2.6.1.9) phosphatransferase).			
DT	HIS8_OR			
DT	Imidazole acetyl			

OS Staphylococcus aureus (strain MN2).
 OC Bacillus; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=196620;
 RV [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagata Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";
 RL Lancet 359:1819-1827(2002).
 RL -1- CATALYTIC ACTIVITY: L-histidinol-phosphate + 2-oxoglutarate
 CC -1- (L-methyl-4-1)-2-oxopropyl phosphate + L-glutamate.
 CC -1- COFACTOR: Pyridoxal phosphate (by similarity).
 CC -1- PATHWAY: Histidine biosynthesis; seventh step.
 CC -1- SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOACYLFRASES. HISTIDINOL-PHOSPHATE AMINOTRANSFERASES
 CC SUPERFAMILY.

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DR ENBL; AF004624; BAB94551.1; -
DR HAMM; MF_01023; -; 1
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR004839; Aminoctransf/2.
DR InterPro; IPR005861; Hisp_amlhotrans.
DR InterPro; IPR001917; Nhltransf_2.
DR Pfam; PF00155; amlnotran_12; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR TIGRfam; TIGR01141; hieC; 1.
DR PROSITE; PS00599; AA_TRANSFMR_CLASS_2; 1.
KW Histidine biosynthesis; Transferase; Aminoctransferase;
KW Pyridoxal phosphate; Complete proteome.
FT BINDING 221 221 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 355 AA; 39846 MW; D6ACC297B67C744 CRC64;

Query Match:	0.54	Score 7,	DB 1,	Length 352;
Best Local Similarity	100.0%	Pred. No. 1.5e+02;		
Matches	7,	Conservative	0;	Mismatches 0;
			Indels	0;
Gaps				0
OY	103	ILFGAGL 109		
Db	83	ILFGAGL 89		
RESULT 75				
TCDS..MOUSE				
ID	TCDS..MOUSE	STANDARD;	PRF;	355 AA.
AC	Q8VDR7;			
DT	15-SEP-2003 (Rel. 42, Created)			
DT	15-SEP-2003 (Rel. 42, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DR	dUDP-D-glucose 4,6-dehydratase (EC 4.2.1.46).			
NN	TCDS.			

05 Mus musculus (Mouse).
06
07 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
08 Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Mus.
09 NCBI_TaxId=10090;
10

RN SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932.
 RA Streusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heston F.,
 RA Dieckman L., Marcusna K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toibynki S., Carninci P., Pringle C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Malkin J.A., Gunaratne P.H.,
 RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murzy D.M., Soedegren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Keltelman M., Machen A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grummond J., Schmutz J., Myers R.M.,
 RA Buterfield A., Schein J.B., Jones S.J.M., Matra M.A.,
 RA Schnerker A., Schein J.B., Jones S.J.M., Matra M.A.,
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC 1-1. CATALYTIC ACTIVITY: dTDP-glucose + dTDP-4-dehydro-6-deoxy-D-
 CC glucose + H(2)O.

CC -1- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY. DTPD-GLUCOSE
CC DEHYDRATASE SUPERFAMILY.
CC -----
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DR EMBL: BC021419; AA#21419.1; -.
DR InterPro: IPR001509; Epimerase_Dh.
DR Pfam: PF01370; Epimerase; 1.
KM lysase; NAD.
SQ SEQUENCE 355 AA; 40598 MW; ABA1913359C266EB CRC64;

Query Match	0.5%;	Score 7;	DB 1;	Length 355;
Best Local Similarity	100.0%;	Pred. No. 1.5e+02;		
Matches 7;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	32	VOLAKEL	38
Db	266	VOLAKEL	272

Search completed: December 18, 2003, 09:12:29
Job time : 29 secs

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OM protein - protein search, using sw model

Run on: December 18, 2003, 09:11:49 : Search time 32 Seconds
(without alignments)
4216.396 Million cell updates/sec

Title: US-09-830-338-1

Perfect score: 1403
Sequence: 1 MATQKASDERISQFDHNL.....SKYTLLOKWLPPSPYIQK 1403

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database:

PIR 76: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	946	67.4	1232	2 A55478	neuronal apoptosis
2	35	2.5	1447	2 T42628	ABC transporter, A
3	9	0.6	210	2 E95198	hypothetical prote
4	9	0.6	414	2 T50010	probable transcrip
5	9	0.6	827	2 H83217	V-ATPase proteolip
6	8	0.6	120	2 T44670	hypothetical prote
7	8	0.6	146	2 F72695	hypothetical prote
8	8	0.6	147	2 H75319	hypothetical prote
9	8	0.6	152	2 C69546	hypothetical prote
10	8	0.6	155	2 T30489	apoptosis inhibito
11	8	0.6	156	2 A70658	transcription term
12	8	0.6	219	2 JCS484	membrane protein c
13	8	0.6	219	2 AP2906	hypothetical prote
14	8	0.6	219	2 G97681	membrane protein c
15	8	0.6	230	2 AB0553	probable deox-Tam1
16	8	0.6	272	2 A43306	daunorubicin biosy
17	8	0.6	290	2 H64306	glycosyl transfera
18	8	0.6	324	2 C41608	hypothetical prote
19	8	0.6	329	2 T27793	hypothetical prote
20	8	0.6	335	2 E69990	proteolase IV homo
21	8	0.6	345	2 C71237	probable transport
22	8	0.6	358	2 T01502	hypothetical prote
23	8	0.6	365	2 A97163	probable GTPase, Y
24	8	0.6	391	2 T34831	acyl-coa dehydroge
25	8	0.6	396	1 A58938	surface protein rh
26	8	0.6	422	2 F75151	hypothetical prote
27	8	0.6	425	2 H71167	probable S-adenosy
28	8	0.6	489	2 F65125	probable general s
29	8	0.6	548	1 A26511	amds protein - Eme

30	8	0.6	824	2 B47301	VARB4 homolog - Bo
31	8	0.6	845	2 T12537	hypothetical prote
32	8	0.6	934	2 T02742	probable ligand-ga
33	8	0.6	1026	2 T03179	probable DNA-dirc
34	8	0.6	1188	2 JC4889	phosphatidylinosit
35	8	0.6	1189	2 JC6118	SH2-containing ino
36	8	0.6	1239	2 S74355	hypothetical prote
37	8	0.6	1280	2 T00365	hypothetical prote
38	8	0.6	1360	2 P96596	hypothetical prote
39	8	0.6	1537	2 F86509	Ct147 hypothetical
40	8	0.6	1537	2 C81558	conserved hypochet
41	8	0.6	1537	2 H72112	ct147 hypothetical
42	7	0.5	45	2 AC0724	hypothetical prote
43	7	0.5	66	2 AF2722	hypothetical prote
44	7	0.5	72	2 C97504	hypothetical prote
45	7	0.5	87	2 T50008	hypothetical prote
46	7	0.5	88	2 A13122	153 family transpo
47	7	0.5	88	2 F98164	insertion element
48	7	0.5	89	2 T35348	probable membrane
49	7	0.5	90	2 B42523	As4L protein - vac
50	7	0.5	97	2 T35051	hypothetical prote
51	7	0.5	103	2 A39980	TYA protein - yeas
52	7	0.5	103	2 C69034	conserved hypochet
53	7	0.5	106	2 F71681	hypothetical prote
54	7	0.5	113	2 A86539	hypothetical prote
55	7	0.5	113	2 T49201	hypothetical prote
56	7	0.5	121	2 H81997	Yajpe-like protei
57	7	0.5	125	2 H81997	probable lipoprote
58	7	0.5	130	2 A82599	conserved hypochet
59	7	0.5	130	2 G57175	hypothetical prote
60	7	0.5	130	2 G57175	hypothetical prote
61	7	0.5	134	2 C65115	hypothetical 15.2
62	7	0.5	134	2 B91142	hypothetical prote
63	7	0.5	137	2 E85987	hypothetical prote
64	7	0.5	137	2 T42327	hypothetical prote
65	7	0.5	140	2 C70223	conserved hypochet
66	7	0.5	145	2 B83611	conserved hypochet
67	7	0.5	149	2 C95319	conserved hypochet
68	7	0.5	152	2 B89947	hypothetical prote
69	7	0.5	155	2 S36662	interleukin-2 - go
70	7	0.5	156	2 H75028	probable H+-transp
71	7	0.5	158	2 D71214	hypothetical prote
72	7	0.5	158	2 G82322	dihydrofolate redu
73	7	0.5	155	2 S73337	hypothetical prote
74	7	0.5	175	2 S69636	hypothetical prote
75	7	0.5	189	2 B49845	hypothetical prote
76	7	0.5	192	2 C97315	uncharacterized pr
77	7	0.5	192	2 A83587	hypothetical prote
78	7	0.5	194	2 G71038	hypothetical prote
79	7	0.5	196	2 B49453	transcription init
80	7	0.5	207	2 G75118	proteasome, chain
81	7	0.5	216	2 A37762	hypothetical prote
82	7	0.5	221	2 A99970	hypothetical prote
83	7	0.5	223	2 H83359	hypothetical prote
84	7	0.5	224	2 S71749	DCL protein precu
85	7	0.5	225	2 C84376	hypothetical prote
86	7	0.5	227	2 A48412	hypothetical prote
87	7	0.5	230	2 S71747	DNA protein precu
88	7	0.5	231	2 G83883	L-ribulose-5-phosp
89	7	0.5	232	2 T09003	response regulator
90	7	0.5	232	2 A27503	testis-specific pr
91	7	0.5	234	2 T30427	probable apoptosis
92	7	0.5	237	2 H90492	ABC transporter, A
93	7	0.5	243	2 AG2169	carbonate dehydrat
94	7	0.5	247	2 C71229	hypothetical prote
95	7	0.5	248	2 G75196	hypothetical prote
96	7	0.5	251	2 C97789	hypothetical prote
97	7	0.5	252	2 F97949	hypothetical prote
98	7	0.5	252	2 B95082	amino acid ABC tra
99	7	0.5	253	2 C72758	probable enoyl-CoA
100	7	0.5	254	2 C72622	hypothetical prote

ALIGNMENTS

RESULT 1
A55478
neural apoptosis inhibitory protein - human
N:Alternate names: NAIP
C:Species: Homo sapiens (man)
C:Date: 05-Jan-1996 #sequence
C:Accession: A55478
R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shuclick, G.; Yaregbi, Z.; Farahani, R.; Baird, S.
Cell 80, 167-178, 1995
A:Title: The gene for neural apoptosis inhibitory protein is partially deleted in indi
A:Reference number: A55478; MIM:95112344; PMID:7613013
A:Accession: A55478
A:Molecule type: mRNA
A:Residues: 1-1232 <ROY>
A:Cross-references: GI:019251
A:Gene: GDB:5MA0, SMA
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A:Map position: 5q12.2-5q13
C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane
P:470-477/Domain: transmembrane #status predicted <TM1>
P:478-496/Domain: nucleotide-binding motif A (P-loop)
P:476/Binding site: ATP (Lys) #status predicted <TM2>
P:618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.4%; Score 946; DB 2; Length 1232;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 MATOQKASDERISOPDNLPELSALGLDAVLAKEEERAKOKGNSQMRSE 60
1 MATOQKASDERISOPDNLPELSALGLDAVLAKEEERAKOKGNSQMRSE 60
61 AKLKTFTYRYSWIFQEMAAAGFYGVSGIOCCGLIFGAGLTRLPJEDHKRF 120
61 AKLKTFTYRYSWIFQEMAAAGFYGVSGIOCCGLIFGAGLTRLPJEDHKRF 120
121 HPDCCGLNKDVGNIYAKYDIRVKLRSRGRKRYQEEARLASFRNPFVQGISPCV 180
121 HPDCCGLNKDVGNIYAKYDIRVKLRSRGRKRYQEEARLASFRNPFVQGISPCV 180
181 LSEAGFVFTGKQDVTVOCCGCLGWEEGDDPWKEHAKWPKCEFLSKSSSEITQYI 240
181 LSEAGFVFTGKQDVTVOCCGCLGWEEGDDPWKEHAKWPKCEFLSKSSSEITQYI 240
241 QSYNGFVDITGEHFNVSQRELPMASAYCNDISIFAYEELRLDSFKDPRRSGAVYALA 300
241 QSYNGFVDITGEHFNVSQRELPMASAYCNDISIFAYEELRLDSFKDPRRSGAVYALA 300
301 KAGLFYTGKDIYVQVSCGGLCKMQGDDPLDHPRCPCPRLQNMKSABVTPLDLS 360
301 KAGLFYTGKDIYVQVSCGGLCKMQGDDPLDHPRCPCPRLQNMKSABVTPLDLS 360
361 RGLICGLLETTSESNSLSDSIYVGPVEMAOGEAKMPOEAKNINLEOLRAAYTSASFRMS 420
361 RGLICGLLETTSESNSLSDSIYVGPVEMAOGEAKMPOEAKNINLEOLRAAYTSASFRMS 420
421 LDDISGDIATHLGCDLSTASRHSKPVQEVLYLPEFNSNLSVVCVGEAGSGKTVLL 480
421 LDDISGDIATHLGCDLSTASRHSKPVQEVLYLPEFNSNLSVVCVGEAGSGKTVLL 480
481 KKIATLWASGCCPLNRFOLVFLSLSTRPDEGLASIIICDLEKESVTEMKRIIYQ 540
481 KKIATLWASGCCPLNRFOLVFLSLSTRPDEGLASIIICDLEKESVTEMKRIIYQ 540
541 QLNQVFLIDYKELCSIPVYGLTQXNHLSTRCLLAATNARADIRRYLETLEIX 600
541 QLNQVFLIDYKELCSIPVYGLTQXNHLSTRCLLAATNARADIRRYLETLEIX 600
600 QLNQVFLIDYKELCSIPVYGLTQXNHLSTRCLLAATNARADIRRYLETLEIX 600

Query 601 AEPFNIVCTILKFLSHNMTLRKFMVFGKQSLQIQTPLEVAALICAHFOYPPDS 660
DB 601 AEPFNIVCTILKFLSHNMTLRKFMVFGKQSLQIQTPLEVAALICAHFOYPPDS 660
Query 661 FDDVAVFKSYMERLSRNKATLILKATVSSCEBALKGFSCCFEPDDDLAAGVDED 720
DB 661 FDDVAVFKSYMERLSRNKATLILKATVSSCEBALKGFSCCFEPDDDLAAGVDED 720
Query 721 EDLTMCMSKFTQRLRPVYFSLSPAFQELAGRLIELDSDQEHODGLYHLKQINS 780
DB 721 EDLTMCMSKFTQRLRPVYFSLSPAFQELAGRLIELDSDQEHODGLYHLKQINS 780
Query 781 PMNTAVANNPNTYSSLPSTKGPRTVSHLHLVDNKESENSENDDYLKHQPEISIQ 840
DB 781 PMNTAVANNPNTYSSLPSTKGPRTVSHLHLVDNKESENSENDDYLKHQPEISIQ 840
Query 841 MQLLGLMQLCPQAVFSMSEHLVLAKTAYQSVTTAACSPPVLQFLQRTLTGALNL 900
DB 841 MQLLGLMQLCPQAVFSMSEHLVLAKTAYQSVTTAACSPPVLQFLQRTLTGALNL 900
Query 901 QYFDHPBSLSLRSIHFPRLGNKTSPPAHFVLETGFDKSGVPTIDQVSAFEPMMW 960
DB 901 QYFDHPBSLSLRSIHFPRLGNKTSPPAHFVLETGFDKSGVPTIDQVSAFEPMMW 960
Query 961 ERNLAEKEDVKSVMQRRASPDLSGTGYSKPKYKPCLEVDVNDIDVVGQDMLETL 1020
DB 961 ERNLAEKEDVKSVMQRRASPDLSGTGYSKPKYKPCLEVDVNDIDVVGQDMLETL 1020
Query 1021 MTPVASORIEHLNHSRGTESIRPALISNAYTKCSISKELSAABEELITLPSIE 1080
DB 1021 MTPVASORIEHLNHSRGTESIRPALISNAYTKCSISKELSAABEELITLPSIE 1080
Query 1081 SLEVGSTIOSDQFPLNDFLCKELSVLEGNINVSYPREFPHHMKELIQTISA 1140
DB 1081 SLEVGSTIOSDQFPLNDFLCKELSVLEGNINVSYPREFPHHMKELIQTISA 1140
Query 1141 EYDPSKLV 1148
DB 1141 EYDPSKLV 1148

RESULT 2
T42628
neural apoptosis inhibitory protein 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence
C:Accession: T42628
R:Faraghi, Z.; Diez, E.; Gros, P.; Mackenzie, A.
Mamm. Genome 10, 761-763, 1999
A:Title: cDNA cloning and the 5' genomic organization of Naip2, a candidate gene for mur
A:Reference number: 223179; MIM:9315342; PMID:10384056
A:Structure: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1447 <YAR>
A:Cross-references: EMBL:AF102871; NID:93860228; PTD:93860229; PTDN:ACJ3002.1
A:Gene: Naip2

Query Match 2.5%; Score 35; DB 2; Length 1447;
Best Local Similarity 100.0%; Pred. No. 26-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

193 DTVOCCSCGCGCLGNWEEGDDPWKEHAKWPKCEFL 227
DB 193 DTVOCCSCGCGCLGNWEEGDDPWKEHAKWPKCEFL 227

RESULT 3
55198
ABC transporter, ATP-binding protein SPI704 [imported] - Streptococcus pneumoniae (strain
C:Species: Streptococcus pneumoniae

C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 11-Jan-2002
 C/Accession: E95198
 R/Retcelin, H.; Neilson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,
 Science 293, 498-506, 2001
 A/Author: Lofthus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A/Reference number: A95000, MUID:21357209, PMID:11465916
 A/Accession: E95198
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-210 <KTR>
 A/Cross-references: GB:AE005672; PIDN:AAK75782.1; PID:g14973198; GSPDB:GN00164; TIGR:SP4
 A/Experimental source: strain TIGR4
 C/Genetics:
 A/Gene: SPI704
 C/Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology
 Query Match 0.6%; Score 9; DB 2; Length 210;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 473 GSGKTVLLK 481
 DB 38 GSGKTVLLK 46
 RESULT 4
 T50010
 Hypothetical protein T31P16.50 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
 C/Accession: T50010
 R/Bevan, M.; Zimmermann, W.; Gruenisen, A.; Wambutt, R.; Kalicki, J.; Woldmann, P.; Sm
 submitted to the Protein Sequence Database, May 2000
 A/Reference number: 225027
 A/Accession: T50010
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-414 <BEV>
 A/Cross-references: EMBL:AJ556332; GSPDB:GN00063; ATSP:T31P16.50
 A/Experimental source: cultivar Columbia; BAC clone T31P16
 C/Genetics:
 A/Gene: ATSP:T31P16.50
 A/Map position: 5
 A/Introns: 55/3; 107/3; 161/1; 207/3; 219/3
 Query Match 0.6%; Score 9; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 34 LAKELEERE 42
 DB 168 LAKELEERE 176
 RESULT 5
 H83217
 Probable transcription regulator PA3420 [imported] - Pseudomonas aeruginosa (strain PA01
 C/Species: Pseudomonas aeruginosa
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C/Accession: H83217
 R/Stover, C.K.; Pham, X.O.; Eyrin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Laddis, K.; Lm,
 Loy, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A/Reference number: A82950; MUID:20431337; PMID:10984043
 A/Accession: H83217
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-827 <STO>

A/Cross-references: GB:AE004763; GB:AE004091; NID:g9949556; PIDN:AG06808.1; GSPDB:GN001;
 A/Experimental source: strain PA01
 C/Genetics:
 A/Gene: PA3420
 Query Match 0.6%; Score 9; DB 2; Length 827;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 472 AGSGKTVLL 480
 DB 42 AGSGKTVLL 50
 RESULT 6
 T44670
 V-ATPase proteolipid [imported] - Desulfohalobium sp. (strain SY) (fragment)
 C/Species: Desulfohalobium sp.
 A/Variety: strain SY
 C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Sep-2000
 C/Accession: T44670
 R/Shibui, H.; Hamamoto, T.; Yoshida, M.; Kagawa, Y.
 Biochem. Biophys. Res. Commun. 234, 341-345, 1997
 A/Title: The stabilizing residues and the functional domains in the hyperthermophilic V-
 A/Reference number: JCS532; MUID:97320421; PMID:9177272
 A/Accession: T44670
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-120 <SHI>
 A/Cross-references: EMBL:U96487; PIDN:AAB64412.1
 A/Experimental source: strain SY
 C/Superfamily: Na-ATPase complex X chain
 Query Match 0.6%; Score 8; DB 2; Length 120;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 103 ILFGAGLT 110
 DB 61 ILFGAGLT 68
 RESULT 7
 F72695
 Hypothetical protein APE0982 - Aeropyrum pernix (strain K1)
 C/Species: Aeropyrum pernix
 C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C/Accession: F72695
 R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatake, Y.; Jin-no, K.; Takah
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DN Res. 6, 83-101, 1999
 A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A/Reference number: A72450; MUID:99310339; PMID:10382966
 A/Accession: F72695
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-146 <KAW>
 A/Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BA79966.1; PID:d1043752; PID:g5104
 A/Experimental source: strain K1
 C/Genetics:
 A/Gene: APE0982
 Query Match 0.6%; Score 8; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 504 LSLSTRP 511
 DB 36 LSLSTRP 43
 RESULT 8
 H75319

hypothetical protein - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C/Accession: H75319

M. J. Shen, M. J. Vanathavan, J. J. Lem, P. J. McDonald, L. J. Uterback, T. J. Zalewski, C. J. Ma
 S. J. Smith, H. O. J. Venter, J. C. J. Fraser, C. M.
 C/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: H75319
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-147 <WHI>
 A/Cross-references: GB:AE002042; GB:AE005513; NID:96459848; PID:AAE11610.1; PID:9645985

A/Experimental source: strain R1
 C/Genetics:
 A/Map position: 1

Query Match

Best Local Similarity 0.6%; Score 8; DB 2; Length 147;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 888 LOGRTLT 895
 DB 109 LOGRTLT 116

RESULT 9

C69546

hypothetical protein AF2371 - Archaeoglobus fulgidus
 C/Species: Archaeoglobus fulgidus
 C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

R. Klenk, H. P. Clayton, R. A. Tomb, J. F. White, O. Nelson, K. E. Ketchum, K. A. Dodson
 G. Glocke, A. J. Zhou, L. J. Overbeck, R. J. Goehry, N. D. J. G. Gill, S. J. Kirschner, E. F.

A/Authors: Uterback, T. J. Cotton, M. D. Spriggs, T. J. Attleach, P. J. Kahne, B. P. Sykes, S.
 A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A/Reference number: A69250; MUID:9809343; PMID:9389475
 A/Accession: C69546
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-152 <KLE>

A/Cross-references: GB:AE001112; GB:AE000782; NID:92689435; PID:AB91296.1; PID:9268972

Query Match

Best Local Similarity 0.6%; Score 8; DB 2; Length 152;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 VPFVSLP 1203
 DB 95 VPFVSLP 102

RESULT 10

T30489

apoptosis inhibitor - Lymantria dispar nuclear polyhedrosis virus
 C/Species: Lymantria dispar nuclear polyhedrosis virus
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

R. Kuzio, J. J. Pearson, M. N. Harwood, S. H. Funk, C. J. Evans, J. T. Slavicek, J. M. Roh
 A/Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d
 A/Reference number: Z20836; MUID:99124785; PMID:9887315
 A/Accession: T30489
 A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA
 A/Residues: 1-155 <KUZ>
 A/Cross-references: EMBL:AF081810; PID:AACT0325.1

Query Match
 Best Local Similarity 0.6%; Score 8; DB 2; Length 155;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 RLAFRNM 169
 DB 7 RLAFRNM 14

RESULT 11

A70658

transcription termination factor nusB [similarity] - Mycobacterium tuberculosis (strain
 W/Alternate names: N utilization substance protein B
 C/Species: Mycobacterium tuberculosis
 C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

R. Cole, S. T. Brogh, R. J. Parkhill, J. J. Garnier, T. J. Churcher, C. J. Harris, D. J. Gordon,
 J. Connor, R. J. Davies, R. J. Devlin, K. J. Feltham, T. J. Gentles, S. J. Hamlin, N. J. Holroyd,
 Rajandream, M. A. J. Rogers, J. J. Rutter, S. J. Seeger, K. J. Skelton, S. J. Squares, S.

A/Authors: Squares, R. J. Sultson, J. B. J. Taylor, K. J. Whitehead, S. J. Barrett, B. G.
 A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom
 A/Reference number: A70500; MUID:98295877; PMID:9634230
 A/Accession: A70658
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-156 <COL>

A/Cross-references: GB:Z8363; GB:AL123456; NID:93261685; PID:CB06175.1; PID:91781069
 A/Experimental source: strain H37Rv
 C/Genetics:
 A/Map position: nusB protein

C/Keywords: transcription termination

Query Match
 Best Local Similarity 0.6%; Score 8; DB 2; Length 156;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AVQAKEL 38
 DB 115 AVQAKEL 122

RESULT 12

JC5484

membrane protein ccmB - Rhizobium etli
 C/Species: Rhizobium etli
 C/Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 20-Aug-1999

R. Aguilera, G. R. J. Soberon, M.
 Gene 182, 129-135, 1998
 A/Title: Cloning and sequence analysis of the Rhizobium etli ccmA and ccmB genes involve
 A/Reference number: JC5483; MUID:97116701; PMID:8982078
 A/Accession: JC5484
 A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA
 A/Residues: 1-219 <AGU>
 A/Cross-references: GB:U28866; NID:91279856; PID:AA840906.1; PID:91279855
 C/Genetics: This protein has six transmembrane regions.
 A/Map position: ccmB

C/Superfamily: cytochrome c biogenesis protein Cym

Query Match
 Best Local Similarity 0.6%; Score 8; DB 2; Length 219;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LSLALGLD 30
 DB 58 LSLALGLD 65

RESULT 13

AF2906
hypothetical protein ccmb [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C/Accession: AF2906
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; PMID:21608550; PMID:11743193
A/Accession: AF2906
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-219 <NR>
A/Cross-references: GB:AB008688; PIDN:AAU4366.1; PID:917741193; GSPDB:GN00186
C/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Map position: circular chromosome
A/Map position: cytochrome c biogenesis protein CycM

Query Match 0.6%; Score 8; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 23 LSALLGMD 30
|||||
58 LSALLGMD 65

RESULT 14

G97681
membrane protein ccmb [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C/Accession: G97681
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, P.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Leppas, C.; Marzella, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; PMID:21608551; PMID:11743194
A/Accession: G97681
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-219 <NR>
A/Cross-references: GB:AB007869; PIDN:AAK8408.1; PID:915157901; GSPDB:GN00169
C/Genetics:
A/Map position: circular chromosome
A/Map position: cytochrome c biogenesis protein CycM

Query Match 0.6%; Score 8; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 23 LSALLGMD 30
|||||
58 LSALLGMD 65

RESULT 15

AB0553
Probable deor-family transcription regulator STY0448 [imported] - Salmonella enterica su
C/Species: Salmonella enterica subsp. enterica serovar Typh
A/Note: this species has also been called Salmonella typh
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AB0553
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davey, R.M.; Dowd, L.; White, N.; Farrar,

, S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A/Authors: Perry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; PMID:21534947; PMID:11677608
A/Accession: AB0553
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-230 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD08866.1; PID:916501679; GSPDB:GN00176
C/Genetics:
A/Map position: STY0448

Query Match 0.6%; Score 8; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 468 VEGRAGSG 475
|||||
51 VEGRAGSG 58

RESULT 16

A43306
daunorubicin biosynthesis regulatory protein dnri [imported] - Streptomyces peucetius
C/Species: Streptomyces peucetius
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C/Accession: A43306
R/Stutzman-Engwall, K.D.; Otten, S.L.; Hutchinson, C.R.
J. Bacteriol. 174, 144-154, 1992
A/Title: Regulation of secondary metabolism in Streptomyces spp. and overproduction of de
A/Reference number: A43306; PMID:92104954; PMID:11729206
A/Accession: A43306
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-272 <STU>
A/Cross-references: GB:M80237; NID:9153242; PIDN:AAA26736.1; PID:9153243
A/Experimental source: ATCC 29050
A/Note: sequence extracted from NCBI backbone (NCBI:75271, NCBI:75272)
C/Keywords: transcription regulation

Query Match 0.6%; Score 8; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 LPELSAL 26
|||||
Db 185 LPELSAL 192

RESULT 17

H64431
glycosyl transferase (EC 2.4.-.-) - Methanococcus jannaschii
C/Species: Methanococcus jannaschii
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 06-Jan-2003
C/Accession: H64431
R/Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodex, A.;
reou, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurest, M.A.
Science 273, 1058-1073, 1996
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A/Reference number: A64300; PMID:96337999; PMID:8688087
A/Accession: H64431
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-290 <BUL>
A/Cross-references: GB:U67549; GB:U77117; NID:91591709; PID:91592318; TIGR:WJ1057; PID:91
C/Genetics:
A/Map position: FOR96513-997385
C/Superfamily: Neisseria meningitidis glycosyl transferase A
C/Keywords: glycosyltransferase

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 290;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1366 LDADIAL 1373
97 LDADIAL 104

RESULT 18

C41608
Hypothetical protein 3 (hima 5' region) - Rhodobacter capsulatus
C/Species: Rhodobacter capsulatus
C/Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 18-Jun-1999
R/Toussaint, B.; Becq, C.; Richard, P.; Colbeau, A.; Vignatier, P.M.
A/Title: A mutation in a Rhodobacter capsulatus gene encoding an integration host factor
A/Accession: C41608
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-324 <TCU>
A/Cross-references: GB:M84030; GB:M62764; NID:G151940; PIDN:AAA26127.1; PID:G151943
C/Superfamily: 3-oxoacyl-lacyl-carrier-protein synthase III

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 324;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 297 AALAKGL 304
233 AALAKGL 240

RESULT 19

T27793
Hypothetical protein ZK228.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
R/Baham, V.
Submitted to the EMBL Data Library, November 1996
A/Accession: T27793
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-329 <WIL>
A/Cross-references: EMBL:Z82086; PIDN:CA804998.1; GSPDB:GN00023; CESP:ZK228.7
A/Genes: CESP:ZK228.7
A/Map position: 5
A/Introns: 107/1; 168/3; 270/1
C/Superfamily: Caenorhabditis hypothetical protein C497.2

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 329;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1072 LLLTLP 1079
249 LLLTLP 256

RESULT 20

E69990
Proteinase IV homolog yrei - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
R/Kumar, P.; Ogatawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet
C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.W.; Chd

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Filtz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gallier
leeh, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.
A/Authors: Lamber, U.; Lazarevic, V.; Lee, S.M.; Levine, M.; Krutka, K.; Lapidus, A.; Lardinois
Y, M.; Ogawa, K.; Ogatawara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetalec
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A/Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, D.; Sekowaka, A.; Serot
T.; Winere, P.; Wipac, A.; Tanaka, T.; Taperia, P.; Tognoni, A.; Tosato, V.; Uchiyama
A/Authors: Yoshikawa, H.F.; Zumbato, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A/Accession: E69990
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-335 <KUN>
A/Cross-references: GB:289119; GB:AL009126; NID:G2635411; PIDN:CB14931.1; PID:G2635437
A/Experimental source: strain 168
A/Genes: yrei

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 335;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1082 LEVSGTQ 1089
63 LEVSGTQ 70

RESULT 21

C71237
Probable transport-ATP binding protein - Pyrococcus horikoshii
C/Species: Pyrococcus horikoshii
C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
R/Kawabuchi, Y.; Sawada, M.; Horikawa, H.; Hikiawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
DNA Res. 5, 55-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A/Reference number: A71000; MUID:98344137; PMID:9679194
A/Accession: C71237
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-345 <KAW>
A/Cross-references: GB:AP000001; NID:G3236128; PIDN:BAA29226.1; PID:G3236543
A/Experimental source: strain OT3
A/Note: This accession replaces an interim accession for a sequence replaced by GenBank
A/Genes: PH0157
C/Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C/Keywords: ATP
F/16-207/Domain: ATP-binding cassette homology <ABC>

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 345;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 473 GSGKTVL 480
36 GSGKTVL 43

RESULT 22

T01902
Hypothetical protein T12H20.10 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 30-Sep-2002
R/Cotton, M.; Graves, T.; Sutterer, C.; Modde, T.
Submitted to the EMBL Data Library, July 1998

A>Description: The sequence of A. thaliana T12H20.
 A:Reference number: 214453
 A:Accession: T01902
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-358 <COT>
 A:Cross-references: EMBL:AF080119; NID:G3600029; PID:g3600031
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Map position: 4
 A:Note: T12H20.10
 C:Superfamily: 2,4-dihydroxyhept-2-ene-1,7

Query Match 0.64; Score 8; DB 2; Length 358;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 LKSRRLRG 152
 DB 80 LKSRRLRG 87

RESULT 23
 A97163
 Probable GTPase, YVAP B, subtilis ortholog [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
 C:Accession: A97163
 R:Moiling, J.; Brelton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J: Bacteriol. 183, 4823-4838, 2001
 A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: A97163
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-365 <KIR>
 A:Cross-references: GB:AE00437; PIDN:AAK80092.1; PID:g15025125; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC7134
 C:Superfamily: yeast probable purine nucleotide-binding protein YBR025C

Query Match 0.64; Score 8; DB 2; Length 365;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 LEEEOKE 45
 DB 249 LEEEOKE 256

RESULT 24
 T34831
 acyl-coa dehydrogenase redw - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
 C:Accession: T34831
 R:O'Leary, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, January 1998
 A:Reference number: 221558
 A:Accession: T34831
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-391 <OIL>
 A:Cross-references: EMBL:AL021530; PIDN:CAA16488.1; GSPDB:GN00070; SCODDB:SC259.20
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: redw; SCODDB:SC259.20
 C:Superfamily: acyl-CoA dehydrogenase

Query Match 0.64; Score 8; DB 2; Length 391;
 Best Local Similarity 100.0%; Pred. No. 29;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LGIDAVQL 34
 DB 334 LGIDAVQL 341

RESULT 25
 A58938
 surface protein rhoptry ROP1 precursor - Toxoplasma gondii
 C:Species: Toxoplasma gondii
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A58938; A45644; S37697
 R:Boothroyd, J.C.
 submitted to GenBank, July 1995
 A:Reference number: A58938
 A:Accession: A58938
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-396 <BOO>
 A:Cross-references: GB:M71274; NID:9897822; PIDN:AAA69859.1; PID:g897823
 A:Note: revision to sequence reported in A45644
 R:Osorio, P.N.; Schwartzman, J.D.; Boothroyd, J.C.
 Mol. Biochem. Parasitol. 50, 1-15, 1992
 A>Title: A Toxoplasma gondii rhoptry protein associated with host cell penetration has w
 A:Reference number: A45644; MUID:92178277; PMID:1542304
 A:Accession: A45644
 A:Molecule type: mRNA
 A:Residues: 'MACRQLGSVNLFPRLDIYCTDPD', 1-352, 'PQR', 358-364, 'R', 366, 'I', 393, 'SP', 396,
 A:Cross-references: EMBL:M71274; NID:g897822
 A:Note: sequence extracted from NCBI backbone (NCBIN:85178, NCBI:P:85179)
 C:Superfamily: surface protein rhoptry
 C:Keywords: surface antigen
 P:1-21/Domain: signal sequence #status predicted <SIG>
 P:22-396/Product: surface protein rhoptry #status predicted <MAT>

Query Match 0.64; Score 8; DB 1; Length 396;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FGAGLTRL 112
 DB 363 FGAGLTRL 370

RESULT 26
 F75151
 hypothetical protein PAB0247 - Pyrococcus abyssi (strain Orsay)
 C:Species: Pyrococcus abyssi
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: F75151
 R:anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A>Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
 A:Reference number: A75001
 A:Accession: F75151
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-422 <KMW>
 A:Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49293.1; PID:g545780;
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: PAB0247
 C:Superfamily: conserved hypothetical protein MJ1095

Query Match 0.64; Score 8; DB 2; Length 422;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1353 LPRILRLN 1360
 DB 38 LPRILRLN 45

RESULT 27

H71167
 Probable S-adenosyl-L-homocysteine hydrolase - Pyrococcus horikoshii
 C/Species: Pyrococcus horikoshii
 C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
 C/Accession: H71167
 R/Kawabuchi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohnuki, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, T.; Kuehida, N.; Oguchi
 DNA Res. 5: 55-76, 1998
 A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
 A/Reference number: A71000; MUID:98344137; PMID:9679194
 A/Accession: H71167
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-425 <KAW>
 A/Cross-references: GB:AP000002; NID:G3336129; PIDN:BAA29629.1; PID:G3256946
 A/Experimental source: strain OT3
 A/Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C/Genetic:
 A/Genes: PH0540
 C/Superfamily: adenosylhomocysteinease

Query Match

0.6%; Score 8; DB 2; Length 425;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 296 VVALAKXG 303
 |||||
 93 VVALAKXG 100

RESULT 28

F65125
 Probable general secretion pathway protein b - Escherichia coli (strain K-12)
 C/Species: Escherichia coli
 C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 C/Accession: F65125
 R/Blaetner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Saeo, Y.
 Science 277, 1453-1462, 1997
 A/Title: The complete genome sequence of Escherichia coli K-12.
 A/Reference number: A64720; MUID:97426617; PMID:9278503
 A/Accession: F65125
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-489 <BLAT>
 A/Cross-references: GB:AE000409; GB:U00096; NID:G1789718; PIDN:AACT6348.1; PID:G1789720;
 A/Experimental source: strain K-12, substrain MG1655
 C/Genetic:
 A/Genes: ynf

Query Match

0.6%; Score 8; DB 2; Length 489;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 470 GEAGSGKT 477
 |||||
 26 GEAGSGKT 33

RESULT 29

A26511
 amds protein - Emoricella nidulans
 C/Species: Emoricella nidulans, Aspergillus nidulans
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
 C/Accession: A26511
 R/Corrick, C.M.; Twomey, A.P.; Hynea, M.J.
 Gene 53, 63-71, 1987
 A/Title: The nucleotide sequence of the amds gene of Aspergillus nidulans and the molecu
 A/Accession: A26511; MUID:87248110; PMID:3036667
 A/Status: preliminary

A/Molecule type: mRNA
 A/Residues: 1-548 <COR>
 A/Cross-references: GB:M6371; NID:9168014; PIDN:AAA33295.1; PID:9168015
 C/Superfamily: amidase

Query Match

0.6%; Score 8; DB 1; Length 548;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 296 VVALAKXG 303
 |||||
 343 VVALAKXG 350

RESULT 30

B47301
 virB4 homolog - Bordetella pertussis
 C/Species: Bordetella pertussis
 C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
 C/Accession: B47301
 R/Weiss, A.A.; Johnson, F.D.; Burns, D.L.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2970-2974, 1993
 A/Title: Molecular characterization of an operon required for pertussis toxin secretion
 A/Reference number: A47301; MUID:93219406; PMID:8464913
 A/Accession: B47301
 A/Status: preliminary
 A/Molecule type: nucleic acid
 A/Residues: 1-824 <WEI>
 A/Note: sequence extracted from NCBI backbone (NCBI:128775, NCBI:128777)
 C/Superfamily: virB4 protein

Query Match

0.6%; Score 8; DB 2; Length 824;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 473 GSGKTVLL 480
 |||||
 459 GSGKTVLL 466

RESULT 31

T12537
 hypothetical protein DKFZp434H244.1 - human (fragments)
 C/Species: Homo sapiens (man)
 C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Nov-2000
 C/Accession: T12537
 R/Kambult, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 Submitted to the Protein Sequence Database, June 1999
 A/Reference number: Z17524
 A/Accession: T12537
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-313/314-845 <WAM>
 A/Cross-references: EMBL:AL096750
 A/Note: the cDNA sequence contains a -1 frameshift near codon 313
 C/Genetic:
 A/Note: DKFZp434H244.1
 C/Superfamily: hypothetical protein YKL215c

Query Match
 0.6%; Score 8; DB 2; Length 845;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 456 PVRFGNN 463
 |||||
 618 PVRFGNN 625

RESULT 32

T02742
 Probable ligand-gated ion channel protein [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein T914.20
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
 C:Accession: T02742; G84692
 R:Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Rod
 submitted to the EMBL Data Library, August 1998
 A:Description: Arabidopsis thaliana chromosome II BAC T914 genomic sequence.
 A:Reference number: Z14710
 A:Accession: T02742
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-934 <R0U>
 A:Cross-references: EMBL:AC005315; NID:G3461834; PID:G3482941
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
 eues, D.; Nieman, M.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: G84692
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-934 <STO>
 A:Cross-references: GB:AE002093; NID:G3482941; PIDN:ACC33239.1; GSPDB:GN00139
 A:Gene: T914.20; At2g29120
 A:Map position: 2
 A:Introns: 69/1; 514/3; 617/1; 748/3

Query Match 0.64; Score 8; DB 2; Length 934;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 939 DKSQVPTI 946
 |||||
 Db 98 DKSQVPTI 105

RESULT 33

T03179
 Probable DNA-directed RNA polymerase (EC 2.7.7.6) largest chain - Chilo iridescent virus
 N:Alternate names: DNA-dependent RNA polymerase
 C:Species: Chilo iridescent virus
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 17-Mar-2000
 C:Accession: T03179
 R:Bahr, U.; Tidona, C.A.; Darai, G.
 Virus Genes 15, 235-245, 1997
 A:Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
 A:Reference number: Z14834; MUID:98141693; PMID:9482589
 A:Accession: T03179
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1026 <BAH>
 A:Cross-references: EMBL:AF003534; NID:G2738385; PIDN:AA94477.1; PID:G2738450
 C:Superfamily: Halobacterium DNA-directed RNA polymerase chain A
 C:Keywords: DNA binding; nucleotidyltransferase; transcription; zinc finger

Query Match 0.64; Score 8; DB 2; Length 1026;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1142 YDPKLVK 1149
 |||||
 Db 993 YDPKLVK 1000

RESULT 34

J04889
 phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase (EC 3.1.3.-) - human
 N:Alternate names: hpi3C5phosphatase
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1996 #sequence_revision 18-Oct-1996 #text_change 05-Nov-1999

C:Accession: J04889; PC4187
 R:Drayer, A.L.; Pessesse, X.; De Smedt, F.; Woscholski, R.; Parker, P.; Erneux, C.
 Biochem. Biophys. Res. Commun. 225, 243-249, 1996
 A:Title: Cloning and expression of a human placenta inositol 1,3,4,5-tetrakisphosphate ar
 A:Reference number: J04889; MUID:96332436; PMID:8769125
 A:Contents: placenta
 A:Accession: J04889
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-1188 <DRA>
 A:Cross-references: EMBL:X98429; NID:G1495455; PIDN:CAM67071.1; PID:e29440; PID:G1495455
 A:Accession: PC4187
 A:Molecule type: protein
 A:Residues: 582-592; 668-675 <DR2>
 C:Comment: This enzyme plays a function in the phosphatidylinositol 3-kinase and inositol
 sequence motifs show that this enzyme interacts with various proteins in signal transduc
 C:Comment: Inositol 1,3,4,5-tetrakisphosphate is also a substrate for this enzyme.
 C:Superfamily: SH2 homology
 C:Keywords: phosphoric monoester hydrolase
 F:5-101/Domain: SH2 homology <SH2>
 F:380/Binding site: substrate (Arg) #status predicted
 F:671/Active site: Cys #status predicted

Query Match 0.64; Score 8; DB 2; Length 1188;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1075 TLPSLESL 1082
 |||||
 Db 226 TLPSLESL 233

RESULT 35

J06118
 SH2-containing inositol phosphatase (EC 3.1.3.-) - mouse
 N:Alternate names: Shc-associated 145K protein
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 12-Feb-1999
 C:Accession: J06118
 R:Damen, J.E.; Liu, L.; Roosen, P.; Humphries, R.K.; Jefferson, A.B.; Majerus, P.W.; Kyte
 Proc. Natl. Acad. Sci. U.S.A. 93, 1689-1693, 1996
 A:Title: The 145-kDa protein induced to associate with Shc by multiple cytokines is an ir
 A:Reference number: J06118; MUID:96202338; PMID:8643691
 A:Accession: J06118
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1189 <DM>
 A:Cross-references: GB:U39203
 A:Experimental source: hemopoietic cell
 C:Comment: This enzyme is a tyrosine-phosphorylated protein. It plays an important role i
 15.

C:Superfamily: SH2 homology
 C:Keywords: cytokine; phosphoric monoester hydrolase
 F:8-104/Domain: SH2 homology <SH2>

Query Match 0.64; Score 8; DB 2; Length 1189;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1075 TLPSLESL 1082
 |||||
 Db 229 TLPSLESL 236

RESULT 36

S74355
 hypothetical protein s110068 - Synecchocystis sp. (strain PCC 6803)
 C:Species: Synecchocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
 C:Accession: S74355
 R:Kamko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, R.; Nakamura, Y.; Miyajima, N.;
 O., K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

C/Accession: H72112
 R/Katman, S.; Mitchell, W.; Marache, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
 Nature Genet. 21, 385-389, 1999
 A/Title: Comparative genomes of *Campylobacter pneumoniae* and *C. trachomatis*.
 A/Reference number: A72000; MUID:99206606; PMID:10192388
 A/Accession: H72112
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1537 <ARN>
 A/Cross-references: GB:AE001602; GB:AE001363; NID:g4376416; PID:RAD18303.1; PID:g437641
 A/Experimental source: strain CML029
 C/Genetics:
 A/Gene: CPN0150

Query Match 0.5%; Score 8; DB 2; Length 1537;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 102 LIFGACL 109
 |||||
 DB 110 LIFGACL 117

RESULT 42
 AC0724
 hypothetical protein STY1940 [imported] - *Salmonella enterica* subsp. *enterica* serovar Ty
 C/Species: *Salmonella enterica* subsp. *enterica* serovar Typh
 A/Note: This species has also been called *Salmonella typhi*
 C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C/Accession: AC0724
 R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
 Ch, T.; Conerton, P.; Cronin, A.; Davis, P.; Davee, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moulé, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
 A/Reference number: AB0502; MUID:21534947; PMID:11677608
 A/Accession: AC0724
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-45 <PAR>
 A/Cross-references: GB:AL513362; PIDN:CAD05493.1; PID:g16502997; GSPDB:GN00176
 C/Genetics:
 A/Gene: STY1940

Query Match 0.5%; Score 7; DB 2; Length 45;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 327 EGDPLD 333
 |||||
 DB 27 EGDPLD 33

RESULT 43
 AF2722
 hypothetical protein Atul184 [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
 C/Species: *Agrobacterium tumefaciens*
 C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C/Accession: AF2722
 R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuyavin, T.; Levy, R.; Li, M.; McCl
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreppan, W.; Perry, M.; Gordon-Kamm,
 Steer, E.W.
 A/Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A/Reference number: AB2577; MUID:21608550; PMID:11743193
 A/Accession: AF2722
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-66 <KUR>
 A/Cross-references: GB:AE008688; PIDN:AA42196.1; PID:g17739587; GSPDB:GN00186

A/Experimental source: strain C58 (Dupont)
 C/Genetics:
 A/Gene: Atul184
 A/Map position: circular chromosome

Query Match 0.5%; Score 7; DB 2; Length 66;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 296 VVALAKA 302
 |||||
 DB 57 VVALAKA 63

RESULT 44
 C97504
 hypothetical protein AGR_C_2188 [imported] - *Agrobacterium tumefaciens* (strain C58, Cerec
 C/Species: *Agrobacterium tumefaciens*
 C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C/Accession: C97504
 R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
 A/Reference number: A97359; MUID:21608551; PMID:11743194
 A/Accession: C97504
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-72 <KUR>
 A/Cross-references: GB:AE007869; PIDN:AAK6988.1; PID:g15156228; GSPDB:GN00169
 C/Genetics:
 A/Gene: AGR_C_2188
 A/Map position: circular chromosome

Query Match 0.5%; Score 7; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 296 VVALAKA 302
 |||||
 DB 63 VVALAKA 69

RESULT 45
 T50008
 hypothetical protein T31P16.30 - *Arabidopsis thaliana*
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
 C/Accession: T50008
 R/Beyan, M.; Zimmermann, W.; Gruenewald, A.; Wambutt, R.; Kalicki, J.; Wöhlmann, F.; Smi
 submitted to the Protein Sequence Database, May 2000
 A/Reference number: Z25027
 A/Accession: T50008
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-87

 A/Cross-references: EMBL:AL556332; GSPDB:GN00063; ATSP:T31P16.30
 A/Experimental source: cultivar Columbia; BAC clone T31P16
 C/Genetics:
 A/Gene: ATSP:T31P16.30
 A/Map position: 5

Query Match 0.5%; Score 7; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 792 LNYVSSL 798
 |||||
 DB 69 LNYVSSL 75

RESULT 46
 AT3122

IS3 family transposase orfA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C/Species: Agrobacterium tumefaciens
 C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C/Accession: A13122
 R/Wood, D.W.; Seubald, J.C.; Kaul, R.; Monke, D.; Chan, L.; Wood, G.E.; Chen, Y.; Mo, L.; Karp, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, S.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A/Author: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A.; Reference number: A82577; MUID:21608550; PMID:11743193
 A/Accession: A13122
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-88 <KTP>
 A/Cross-references: GB:A808689; PIDN:AAL45399.1; PID:g17743097; GSPDB:GN00187
 A/Experimental source: strain C58 (Dupont)
 C/Genetics:
 A/Map position: linear chromosome

Query Match 0.5%; Score 7; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 59 SEAKRLK 65
 |||||
 Db 51 SEAKRLK 57

RESULT 47
 P98164
 Insertion element ISr1 hypothetical 10K protein A3 [imported] - Agrobacterium tumefaciens
 C/Species: Agrobacterium tumefaciens
 C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
 C/Accession: P98164
 R/Goodner, B.; Hinkle, G.; Galtung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman, A.; Liu, F.; Wollem, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A/Reference number: A97359; MUID:21608551; PMID:11743194
 A/Accession: P98164
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-88 <KTP>
 A/Cross-references: GB:A807870; PIDN:AAK8840.1; PID:g15186602; GSPDB:GN00170
 A/Genetic: AGR_L_545
 A/Map position: linear chromosome

Query Match 0.5%; Score 7; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 59 SEAKRLK 65
 |||||
 Db 51 SEAKRLK 57

RESULT 48
 T35348
 Probable membrane protein - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
 C/Accession: T35348
 R/Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 Submitted to the EMBL Data Library, May 1999
 A/Reference number: Z21575
 A/Accession: T35348
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-89 <OLI>

A/Cross-references: EMBL:AL049863; PIDN:CA842957.1; GSPDB:GN00070; SCOEDB:SCSH1.32
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Genetic: SCOEDB:SCSH1.32

Query Match 0.5%; Score 7; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 293 AVGVALL 299
 |||||
 Db 74 AVGVALL 80

RESULT 49
 B42523
 A54L protein - vaccinia virus (strains WR and Copenhagen)
 A/Alternate names: Saipd protein
 C/Species: vaccinia virus
 A/Note: host Homo sapiens (man)
 C/Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 07-May-1999
 C/Accession: B42523; J01825
 R/Johnson, G.P.
 Submitted to GenBank, June 1990
 A/Reference number: A33172
 A/Accession: B42523
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-90 <JOH>
 R/Smith, G.L.; Chan, Y.S.; Howard, S.T.
 J. Gen. Virol. 72, 1349-1376, 1991
 A/Title: Nucleotide sequence of 42kbp of vaccinia virus strain WR from near the right arm
 A/Reference number: J01767; MUID:91259063; PMID:2045793
 A/Accession: J01825
 A/Molecule type: DNA
 A/Residues: 1-90 <SMI>
 A/Cross-references: DDBJ:D11079

Query Match 0.5%; Score 7; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1269 SFFKTLN 1275
 |||||
 Db 43 SFFKTLN 49

RESULT 50
 T35051
 Hypothetical protein SC4G2.16c SC4G2.16c - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
 C/Accession: T35051
 R/Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 Submitted to the EMBL Data Library, August 1998
 A/Reference number: Z21566
 A/Accession: T35051
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-97 <SEE>
 A/Cross-references: EMBL:AL031371; PIDN:CAA20553.1; GSPDB:GN00070; SCOEDB:SC4G2.16c
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Genetic: SCOEDB:SC4G2.16c

Query Match 0.5%; Score 7; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 717 VDEEDL 723
 |||||
 Db 18 VDEEDL 24

RESULT 51

A39980
 C:Species: Saccharomyces cerevisiae
 C:Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 20-Sep-1999
 C:Accession: A39980
 R:Liaw, X.B.; Clare, J.J.; Parahaugh, P.J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 8520-8524, 1987
 A:Title: The upstream activation site of a Ty2 element of yeast is necessary but not sufficient for Ty2 activation
 A:Reference number: A39980; MUID:88068620; PMID:2825192
 A:Accession: A39980
 A:Molecule type: DNA
 A:Residues: 1-103 <LTA>
 A:Cross-references: GB:M18805; NID:g173114; PIDN:AAA5187.1; PID:g173115
 C:Genetics:
 A:Mobile element: retrotransposon Ty2.917
 C:Superfamily: Ty2 protein

Query Match 0.5%; Score 7; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 QNSPNLH 1158
 |||||
 DB 8 QNSPNLH 14

RESULT 52

C69034
 conserved hypotheoretical protein MTH1251 - Methanobacterium thermoautotrophicum (strain Delta H)
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: C69034
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicalaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwant, N.; K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional analysis
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: C69034
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-103 <MTH>
 A:Cross-references: GB:AE000891; GB:AE000666; NID:g2622345; PIDN:AA85740.1; PID:g262234
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH1251

Query Match 0.5%; Score 7; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 683 ELKATV 689
 |||||
 DB 19 ELKATV 25

RESULT 53

F71681
 hypotheoretical protein RP266 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
 C:Accession: F71681
 R:Anderson, S.G.R.; Zomrodipour, A.; Andersen, J.O.; Sichteritz-Ponten, T.; Almark, U.
 Nature 396, 133-140, 1998
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A:Reference number: A71630; MUID:99039499; PMID:9823893
 A:Accession: F71681
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-106 <AND>
 A:Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14728.1; PID:g3868682

A:Experimental source: strain Madrid E
 C:Genetics:
 A:Gene: RP266

Query Match 0.5%; Score 7; DB 2; Length 106;
 Best Local Similarity 100.0%; Pred. No. 98;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 477 TVLKKI 483
 |||||
 DB 98 TVLKKI 104

RESULT 54

A85639
 hypotheoretical protein Z1446 (imported) - Escherichia coli (strain O157:H7, substrain EDL93)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: A85639
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.; Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Diallanta, K.; Apodaca, J.; Bowers, V.; Wurmach, E.; Drzonek, H.; Ansojge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.; et al.
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: A85639
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-113 <STO>
 A:Cross-references: GB:AE005174; NID:g12514299; PIDN:AA655573.1; GSPDB:GN00145; UMGF:Z1446
 A:Experimental source: strain O157:H7, substrain EDL93
 C:Genetics:
 A:Gene: Z1446

Query Match 0.5%; Score 7; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1040 FIESIRP 1046
 |||||
 DB 18 FIESIRP 24

RESULT 55

T49201
 Y-type-like protein - Arabidopsis thaliana
 N:Alternate names: protein P27K19.70
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
 C:Accession: T49201
 R:Benes, V.; Wurmach, E.; Drzonek, H.; Ansojge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.; et al.
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z25014
 A:Accession: T49201
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-121 <BEN>
 A:Cross-references: EMBL:AL163832; GSPDB:GN00061; ATSP:F27K19.70
 A:Experimental source: cultivar Columbia; BAC clone F27K19
 A:Map position: 3
 A:Introns: 32/3; 47/2; 83/3; 102/2

Query Match 0.5%; Score 7; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1109 VDLGGNI 1115
 |||||
 DB 7 VDLGGNI 13

RESULT 56

H81997
 Probable lipoprotein NMA0065 [Imported] - Neisseria meningitidis (strain Z2491 serogroup C)
 C/Species: Neisseria meningitidis
 C/Date: 05-May-2000 #sequence_rev10n 05-May-2000 #text_change 02-Feb-2001
 A/Accession: H81997
 R/Author: J. Achtman, M. James, K.D. Bentley, S.D. Churcher, C. Klee, S.R. Morel, J. Holtz, S. Jorgensen, K. Leather, S. Mout, S. Mungall, K. Quail, M.A. Rajandream, Nature 406, 502-506, 2000
 A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A/Reference number: A81775; MUID:20222556; PMID:10761919
 A/Accession: H81997
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-125 <PAR>
 A/Cross-references: GB:A162752; GB:A157959; NID:G7378778; PIDN:CA83381.1; PID:G737883
 A/Experimental source: serogroup A, strain Z2491
 C/Genetics: NMA0065
 C/Superfamily: Neisseria meningitidis probable lipoprotein NMA0065

Query Match
 Best Local Similarity 0.5%; Score 7; DB 2; Length 125;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 LSALLGL 29
 |||||
 9 LSALLGL 15

RESULT 57
 F81226
 lipoprotein, probable NMB0204 [Imported] - Neisseria meningitidis (strain MCS8 serogroup C)
 C/Species: Neisseria meningitidis
 C/Date: 31-Mar-2000 #sequence_rev10n 31-Mar-2000 #text_change 19-Jun-2001
 A/Accession: F81226
 R/Author: H. Saunders, N.J. Heidelberg, J. Jeffries, A.C. Nelson, K.R. Eisen, J.R. Hickley, E.K. Haft, D.H. Salberg, S.L. White, O. Fleischmann, R.D. Dougherty, B.A. Science 287, 1809-1815, 2000
 A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
 A/Reference number: A81000; MUID:20175755; PMID:10710307
 A/Accession: F81226
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-125 <TEXT>
 A/Cross-references: GB:A8002377; GB:A8002098; NID:G7225416; PIDN:AA40661.1; PID:G722542
 A/Experimental source: serogroup B, strain MCS8
 C/Genetics: NMB0204
 C/Superfamily: Neisseria meningitidis probable lipoprotein NMA0065

Query Match
 Best Local Similarity 0.5%; Score 7; DB 2; Length 125;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 LSALLGL 29
 |||||
 9 LSALLGL 15

RESULT 58
 A82599
 conserved hypothetical protein X2112 [Imported] - Xylella fastidiosa (strain 9A5C)
 C/Species: Xylella fastidiosa
 C/Date: 18-Aug-2000 #sequence_rev10n 20-Aug-2000 #text_change 20-Aug-2000
 A/Accession: A82599
 R/Author: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing, Nature 406, 151-157, 2000
 A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A/Reference number: A82515; MUID:20355717; PMID:10910347
 A/Note: for a complete list of authors see reference number A59328 below
 A/Accession: A82599

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-130 <SIM>
 A/Cross-references: GB:A8004026; GB:A8003849; NID:G9107228; PIDN:AA804911.1; GSPDB:GN001
 A/Experimental source: strain 9A5C
 R/Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abrão, F.A.; Agencio, M.; Alvares, R.; Azeiteiro, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carter, H. submitted to Genbank, June 2000
 A/Author: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laigret, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.; Rodrigues, V.; Rosa, A.J.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A/Reference number: A59328
 A/Contents: annotation
 C/Genetics: A59328
 A/Gene: X2112

Query Match
 Best Local Similarity 0.5%; Score 7; DB 2; Length 130;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 SALGLD 30
 |||||
 31 SALGLD 37

RESULT 59
 G75175
 Hypothetical protein PAB0387 - Pyrococcus abyssi (strain Orsay)
 C/Species: Pyrococcus abyssi
 C/Date: 20-Aug-1999 #sequence_rev10n 20-Aug-1999 #text_change 20-Aug-1999
 A/Accession: G75175
 R/Author: Genoscope submitted to the EMBL Data Library, July 1999
 A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
 A/Reference number: A75001
 A/Accession: G75175
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-130 <RAW>
 A/Cross-references: GB:A7248284; GB:A7096636; NID:G5457730; PIDN:CA849486.1; PID:G1515381
 A/Experimental source: strain Orsay
 C/Genetics: PAB0387
 A/Gene: PAB0387

Query Match
 Best Local Similarity 0.5%; Score 7; DB 2; Length 130;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 LAKELEE 40
 |||||
 29 LAKELEE 35

RESULT 60
 G65115
 hypothetical 15.2 kD protein in rplM-hba intergenic region - Escherichia coli (strain K-12)
 C/Species: Escherichia coli
 C/Date: 12-Sep-1997 #sequence_rev10n 17-Sep-1997 #text_change 01-Mar-2002
 A/Accession: G65115
 R/Author: F.R. Plunkett III, G. Bloch, C.A. Perna, N.T. Burland, V. Riley, M. Col A/Authors: Rose, D.J.; Mau, B.; Sha, Y. Science 277, 1453-1462, 1997
 A/Title: The complete genome sequence of Escherichia coli K-12.
 A/Reference number: A64720; MUID:97426617; PMID:9278503
 A/Accession: G65115
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA

A:Residues: 1-134 <BLAT>
A:Cross-references: GB:AB000402; GB:U00096; NID:G1789619; PIDN:AACT6265.1; PID:G1789628;
A:Experimental source: strain K-12, substrain MG1655
A:Gene: yhcB
A:Genetics:
C:Superfamily: hypothetical protein H1628

Query Match 0.5%; Score 7; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LPELSA 25
|||||
DB 86 LPELSA 92

RESULT 61

hypothetical protein Eca4106 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: B91142

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Ganawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: B91142

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-134 <HAY>

A:Cross-references: GB:BA000007; PIDN:BAJ37529.1; PID:G13363579; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain R1MD 0509952

A:Genetics:

A:Gene: Eca4106

C:Superfamily: hypothetical protein H1628

Query Match 0.5%; Score 7; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LPELSA 25
|||||
DB 86 LPELSA 92

RESULT 62

hypothetical protein yhcB [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: B85987

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potlowski, K.; Apodaca,
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5460; MUID:21074935; PMID:11206551

A:Accession: B85987

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-134 <STO>

A:Cross-references: GB:AE005174; NID:G12517854; PIDN:AA658361.1; GSPDB:GN00145; UMGF:245

A:Experimental source: strain O157:H7, substrain EDL933

A:Genetics:

A:Gene: yhcB

C:Superfamily: hypothetical protein H1628

Query Match 0.5%; Score 7; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LPELSA 25
|||||

DB 86 LPELSA 92

RESULT 63

hypothetical protein - phage SPPI

C:Species: phage SPPI

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000

C:Accession: T42327

R:Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997

A:Title: The complete nucleotide sequence and functional organization of Bacillus subtilis

A:Reference number: 222137; MUID:98094274; PMID:9431185

A:Accession: T42327

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-137 <ALO>

A:Cross-references: EMBL:X97918; PIDN:CAA6534.1

Query Match 0.5%; Score 7; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1115 INVSVI 1121
|||||
DB 37 INVSVI 43

RESULT 64

conserved hypothetical protein BBD15 - Lyme disease spirochete plasmid D/1p17

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C:Accession: C70223

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,

son, D.; Peterson, J.; Klevavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,

Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943; PMID:9403685

A:Accession: C70223

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-140 <KLE>

A:Cross-references: GB:AE000793; NID:G2689927; PIDN:AA66348.1; PID:G2689934; TIGR:BBD15

A:Experimental source: strain B31

A:Genetics:

A:Gene: plasmid

Query Match 0.5%; Score 7; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 LGCDLST 440
|||||
DB 62 LGCDLST 68

RESULT 65

conserved hypothetical protein PA0269 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: B83611

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brj

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.. Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog

A:Reference number: AB2950; MUID:20437337; PMID:10984043

A:Accession: B83611

A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-145 <STO>
 A:Cross-references: GB:AE004465; GB:AE004091; NID:g9946107; PIDN:AA03658.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA0269

Query Match 0.5% Score 7; DB 2; Length 145;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 298 ALAKAGL 304
 DB 24 ALAKAGL 30

RESULT 66
 C95319
 conserved hypothetical protein Sma0841 [imported] - Sinorhizobium meliloti (strain 1021)
 C:Species: Sinorhizobium meliloti
 C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: C95319
 R:Barrett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: C95319
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-149 <KUR>
 A:Cross-references: GB:AE006469; PIDN:AAK65117.1; PID:g14523555; GSPDB:GN00165
 R:Experimental source: strain 1021, megaplasmid pSymA
 R:Gallibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 P.; Chailin, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.;
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kahan, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure,
 hebaull, P.; Vandenbol, M.; Vornholter, F.J.; Weidner, S.; Weller, D.H.; Wong, K.; Yen, K.
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: Sma0841
 A:Genome: plasmid

Query Match 0.5% Score 7; DB 2; Length 149;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 59 SEAKRUK 65
 DB 102 SEAKRUK 108

RESULT 67
 B89947
 hypothetical protein SA1469 [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 14-Apr-2003
 C:Accession: B89947
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: B89947
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-152 <KUR>
 A:Cross-references: GB:BA000018; PID:g13701441; PIDN:BA842735.1; GSPDB:GN00149
 A:Experimental source: strain N315

C:Genetics:
 A:Gene: SA1469
 C:Superfamily: uncharacterized protein with an ACT domain

Query Match 0.5% Score 7; DB 2; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1060 ISKRLKS 1066
 DB 94 ISKRLKS 100

RESULT 68
 S38662
 interleukin-2 - goat
 C:Species: Capra aegagrus hircus (domestic goat)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
 C:Accession: S38662
 R:Rimstad, B.
 Submitted to the EMBL Data Library, November 1993
 A:Description: The molecular cloning and expression of caprine interleukin 2.
 A:Reference number: S38662
 A:Accession: S38662
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-155 <RTM>
 A:Cross-references: EMBL:X76063; NID:g416002; PIDN:CA53664.1; PID:g416003
 C:Superfamily: Interleukin-2

Query Match 0.5% Score 7; DB 2; Length 155;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1294 LEMTKLS 1300
 DB 51 LEMTKLS 57

RESULT 69
 H75028
 Probable H+-transporting two-sector ATPase (EC 3.6.3.14) proteolipid chain PAB1181 - Pyr
 C:Species: Pyrococcus abyssi
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 03-Jun-2002
 C:Accession: H75028
 R:Anonymous, Genoscope
 Submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
 A:Reference number: A75001
 A:Accession: H75028
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-158 <KAM>
 A:Cross-references: GB:UJ248288; GB:AL096836; NID:g5458960; PIDN:CA50670.1; PID:g545918
 A:Experimental source: strain Oxeay
 C:Genetics:
 A:Gene: PAB1181
 C:Superfamily: Na+-ATPase complex K chain
 C:Keywords: hydrolase

Query Match 0.5% Score 7; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 103 ILFGAGL 109
 DB 94 ILFGAGL 100

RESULT 70
 D71214
 hypothetical protein PH1980 - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii

C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C/Accession: D71214
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hakawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohnuki, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A/Reference number: A71000; MUID:98344137; PMID:9679194
A/Accession: D71214
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-162 <KAW>
A/Cross-references: GB:AP000007; NID:G3236134; PIDN:BA31107.1; PID:G3258424
A/Experimental source: strain OT3
A/Note: this accession replaces an interim accession for a sequence replaced by GenBank
C/Genetics:
A/Gene: PH1980
C/Superfamily: Na+-ATPase complex K chain

Query Match 0.5%; Score 7; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 ILPGAGL 109
|||||
DB 98 ILPGAGL 104

RESULT 71
dh2322
dh2322
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C/Accession: G82322
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, M.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Charadon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bae, S.; Qin, H.; Dragol, I.; Sellers, F.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: G82322
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-165 <HEI>
A/Cross-references: GB:AE004131; GB:AE003952; NID:G9654856; PIDN:AAF93613.1; GSPDB:GN001
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC0440
A/Map position: 1
C/Superfamily: type I dihydrofolate reductase; type I dihydrofolate reductase homology

Query Match 0.5%; Score 7; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 297 AALAKAG 303
|||||
DB 82 AALAKAG 88

RESULT 72
S73337
hypothetical protein E07_orf175 - Mycoplasma pneumoniae (strain ATCC 29342)
C/Species: Mycoplasma pneumoniae
A/Variety: ATCC 29342
C/Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C/Accession: S73337
R:Himmelreich, R.; Hilbert, H.; Piagens, H.; Pirkl, E.; Li, B.-C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A/Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A/Reference number: S73337; MUID:97105885; PMID:8948633
A/Accession: S73337
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA

A/Residues: 1-175 <HIM>
A/Cross-references: EMBL:AE000002; GB:U00089; NID:G1673651; PIDN:AA895659.1; PID:G167365.
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C/Genetics:
A/Genetic code: GCC3
C/Superfamily: Mycoplasma pneumoniae hypothetical protein E07_orf175

Query Match 0.5%; Score 7; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 523 LLEKEGS 529
|||||
DB 61 LLEKEGS 67

RESULT 73
S69636
hypothetical protein YDR469w - yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
C/Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002
C/Accession: S69636
R:Dietrich, F.S.
submitted to the EMBL Data Library, August 1995
A/Description: The sequence of S. cerevisiae cosmid 9410, 8035, 8166, and 9787.
A/Reference number: S69554
A/Accession: S69636
A/Molecule type: DNA
A/Residues: 1-175 <DIE>
A/Cross-references: EMBL:U03050; NID:G927726; PID:G927731; GSPDB:GN00004; MIPS:YDR469w
C/Genetics:
A/Gene: SGD:SDC1; MIPS:YDR469w
A/Cross-references: SGD:S0002877
A/Map position: 48
C/Superfamily: Saccharomyces hypothetical protein YDR469w

Query Match 0.5%; Score 7; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 751 LAGMKLI 757
|||||
DB 135 LAGMKLI 141

RESULT 74
T49816
hypothetical protein B24H17.20 [imported] - Neurospora crassa
C/Species: Neurospora crassa
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C/Accession: T49816
R:Schulte, U.; Altm, V.; Hohnsbeil, J.; Brandt, P.; Fartmann, B.; Holland, R.; Watakura,
submitted to the Protein Sequence Database, May 2000
A/Reference number: Z25022
A/Accession: T49816
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-177 <SCH>
A/Cross-references: EMBL:AL356815; GSPDB:GN00116; NCSP:B24H17.20
A/Experimental source: BAC clone B24H17; strain OR74A
C/Genetics:
A/Gene: NCSP:B24H17.20
A/Map position: 6

Query Match 0.5%; Score 7; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 EEBEOKB 45
|||||
DB 136 EEBEOKB 142

RESULT 75
B49845
hypothetical protein A (hema 5' region) - Rhodobacter sphaeroides
C:Species: Rhodobacter sphaeroides
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: B49845
R:Neidle, E.L.; Kaplan, S.
J. Bacteriol. 175, 2292-2303, 1993
A:Title: Expression of the Rhodobacter sphaeroides hema and hemT genes, encoding two 5-kDa heme biosynthetic enzymes
A:Reference number: A49845; MUID:93224431; PMID:8468290
A:Contents: 2,41
A:Accession: B49845
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1189 <NEI>
A:Cross-references: GB:L07490; NID:G151936; PIRN:AA72324.1; PID:G457150
A:Note: sequence extracted from NCBI backbone (NCBIN:129178, NCBI:P:129179)
C:Superfamily: Rhodobacter sphaeroides hypothetical protein A (hema 5' region)

Query Match 0.54; Score 7; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 PDEGLAS 517
|||||
Db 72 PDEGLAS 78

Search completed: December 18, 2003, 09:15:39
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using 6w model

Run on: December 18, 2003, 09:15:05 ; Search time 285 Seconds
(without alignments)
919.377 Million cell updates/sec

Title: US-09-830-338-1

Sequence: 1403
1 MATOOKASDERISQFDHNL.....SKYLTILQKILFSPRIQK 1403

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 696363 segs, 186758610 residues

Word size : 0

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppa/PCN_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppa/PCRN_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppa/US09C_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppa/US10C_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1403	100.0	1403	8	US-08-913-322-22
2	1403	100.0	1403	8	US-08-913-322-24
3	1403	100.0	1403	15	US-10-285-408-1
4	496	35.4	782	9	US-09-841-739-9
5	496	35.4	782	12	US-10-449-315-9
6	385	27.4	385	12	US-10-029-386-33707
7	203	14.5	203	12	US-10-029-386-33933
8	75	5.3	118	9	US-09-925-299-1033
9	75	5.3	118	11	US-09-925-299-1033
10	50	3.6	50	15	US-10-138-618-26
11	47	3.3	47	15	US-10-138-618-13
12	22	1.6	37	9	US-09-864-761-47337
13	12	0.9	898	9	US-09-841-739-11
14	12	0.9	898	12	US-10-449-315-11
15	8	0.6	15	9	US-09-812-471-20

16	8	0.6	15	10	US-09-812-633-20	Sequence 20, Appl
17	8	0.6	15	10	US-09-888-117-20	Sequence 20, Appl
18	8	0.6	64	12	US-09-933-767-580	Sequence 580, Appl
19	8	0.6	64	15	US-10-023-282-580	Sequence 580, Appl
20	8	0.6	68	10	US-09-201-936-16	Sequence 16, Appl
21	8	0.6	95	9	US-09-925-297-743	Sequence 743, Appl
22	8	0.6	201	15	US-10-156-761-8837	Sequence 8837, Ap
23	8	0.6	259	9	US-09-925-299-821	Sequence 821, Appl
24	8	0.6	259	11	US-09-925-299-821	Sequence 821, Appl
25	8	0.6	481	15	US-10-156-761-12012	Sequence 12012, A
26	8	0.6	496	10	US-09-974-592-10	Sequence 10, Appl
27	8	0.6	496	10	US-09-201-936-10	Sequence 10, Appl
28	8	0.6	567	12	US-09-933-767-573	Sequence 573, Appl
29	8	0.6	567	15	US-10-023-282-573	Sequence 573, Appl
30	8	0.6	667	9	US-09-896-852-55	Sequence 55, Appl
31	8	0.6	667	11	US-09-728-644-55	Sequence 55, Appl
32	8	0.6	976	10	US-09-969-528-2	Sequence 2, Appl
33	8	0.5	7	12	US-10-291-607-15	Sequence 15, Appl
34	7	0.5	10	9	US-09-812-471-15	Sequence 15, Appl
35	7	0.5	10	10	US-09-812-633-15	Sequence 15, Appl
36	7	0.5	10	10	US-09-988-117-15	Sequence 15, Appl
37	7	0.5	14	9	US-09-812-471-14	Sequence 14, Appl
38	7	0.5	14	10	US-09-812-633-14	Sequence 14, Appl
39	7	0.5	14	10	US-09-988-117-14	Sequence 14, Appl
40	7	0.5	16	9	US-09-812-471-13	Sequence 13, Appl
41	7	0.5	16	10	US-09-812-633-13	Sequence 13, Appl
42	7	0.5	16	10	US-09-988-117-13	Sequence 13, Appl
43	7	0.5	20	9	US-09-812-471-10	Sequence 10, Appl
44	7	0.5	20	10	US-09-812-633-10	Sequence 10, Appl
45	7	0.5	20	10	US-09-988-117-10	Sequence 10, Appl
46	7	0.5	42	9	US-09-726-643-145	Sequence 145, Appl
47	7	0.5	42	14	US-10-042-131-145	Sequence 145, Appl
48	7	0.5	48	12	US-10-232-286-9	Sequence 9, Appl
49	7	0.5	50	10	US-09-071-818-94	Sequence 94, Appl
50	7	0.5	50	15	US-10-138-618-22	Sequence 22, Appl
51	7	0.5	50	15	US-10-138-618-22	Sequence 22, Appl
52	7	0.5	50	15	US-10-138-618-31	Sequence 31, Appl
53	7	0.5	50	15	US-10-213-512-94	Sequence 94, Appl
54	7	0.5	52	9	US-09-864-761-41562	Sequence 41562, A
55	7	0.5	56	9	US-09-864-761-47236	Sequence 47236, A
56	7	0.5	56	15	US-10-156-761-8239	Sequence 8239, Appl
57	7	0.5	56	15	US-10-156-761-8496	Sequence 8496, Appl
58	7	0.5	64	9	US-09-864-761-46549	Sequence 46549, A
59	7	0.5	66	9	US-09-864-761-43318	Sequence 43318, A
60	7	0.5	67	10	US-09-201-936-23	Sequence 23, Appl
61	7	0.5	68	10	US-09-201-936-27	Sequence 27, Appl
62	7	0.5	68	15	US-10-041-859-15	Sequence 15, Appl
63	7	0.5	68	15	US-10-041-859-16	Sequence 16, Appl
64	7	0.5	69	9	US-09-864-761-44802	Sequence 44802, A
65	7	0.5	84	15	US-10-106-698-4797	Sequence 4797, Appl
66	7	0.5	91	12	US-10-029-386-30446	Sequence 30446, A
67	7	0.5	99	9	US-09-864-761-38294	Sequence 38294, A
68	7	0.5	101	9	US-09-864-761-34814	Sequence 34814, A
69	7	0.5	102	9	US-09-864-761-39550	Sequence 39550, A
70	7	0.5	107	15	US-10-156-761-8010	Sequence 8010, Appl
71	7	0.5	109	9	US-09-867-550-1404	Sequence 1404, Appl
72	7	0.5	130	12	US-10-029-386-32869	Sequence 32869, A
73	7	0.5	134	12	US-10-287-274-415	Sequence 415, Appl
74	7	0.5	139	9	US-09-815-242-5364	Sequence 5364, Appl
75	7	0.5	144	15	US-10-156-761-14388	Sequence 14388, A
76	7	0.5	152	9	US-09-815-242-12642	Sequence 12642, A
77	7	0.5	152	9	US-09-815-242-12879	Sequence 12879, A
78	7	0.5	172	15	US-10-041-859-9	Sequence 9, Appl
79	7	0.5	172	15	US-10-041-859-9	Sequence 9, Appl
80	7	0.5	180	15	US-10-156-761-8894	Sequence 8894, Appl
81	7	0.5	197	15	US-10-157-031-367	Sequence 367, Appl
82	7	0.5	198	9	US-09-925-301-1184	Sequence 1184, Appl
83	7	0.5	198	15	US-10-106-698-5870	Sequence 5870, Appl
84	7	0.5	202	11	US-09-791-279-1590	Sequence 1590, Appl
85	7	0.5	207	9	US-09-925-301-1160	Sequence 1160, Appl
86	7	0.5	209	9	US-09-925-301-931	Sequence 931, Appl
87	7	0.5	222	12	US-10-091-007-58	Sequence 58, Appl
88	7	0.5	234	9	US-09-764-998-202	Sequence 202, Appl

69	7	0.5	240	10	US-09-908-193-43	Sequence 43, App1
90	7	0.5	240	11	US-09-823-187-74	Sequence 74, App1
91	7	0.5	245	15	US-10-158-761-8594	Sequence 8594, App
92	7	0.5	249	15	US-10-158-761-14452	Sequence 14452, App
93	7	0.5	255	15	US-10-203-708-45	Sequence 45, App1
94	7	0.5	258	15	US-10-158-761-9957	Sequence 9957, App
95	7	0.5	259	15	US-10-029-386-32237	Sequence 32237, App
96	7	0.5	260	15	US-10-102-806-503	Sequence 503, App
97	7	0.5	265	5	US-09-726-643-10218	Sequence 10218, App
98	7	0.5	267	9	US-10-042-141-143	Sequence 143, App
99	7	0.5	267	14	US-10-259-165-174	Sequence 174, App
100	7	0.5	280	12		

ALIGNMENTS

RESULT 1

US-08-913-322-22

Sequence 22, Application US/08913322

Publication No. US20020137028A1

GENERAL INFORMATION:

APPLICANT: Korneljuk, Robert G.

APPLICANT: MacKenzie, Alexander E.

APPLICANT: Roy, Natalie

APPLICANT: Robertson, George

APPLICANT: Tama, Katu

TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INHIBITOR

FILE REFERENCE: 07891/01501

CURRENT APPLICATION NUMBER: US/08/913,322

EARLIER FILING DATE: 1997-09-12

EARLIER APPLICATION NUMBER: PCT/IB97/00142

EARLIER FILING DATE: 1997-01-17

EARLIER APPLICATION NUMBER: GB 9601108.5

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 22

LENGTH: 1403

TYPE: PRT

ORGANISM: Homo sapiens

US-08-913-322-22

Query Match

Best Local Similarity 100.0%; Score 1403; DB 8; Length 1403;

Matches 1403; Consecutive 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MATQKASDERISQFDHNLPELSALLGLDAVQAKLEEEBOKERAKKQKYNQKMSSE	60
Db	1	MATQKASDERISQFDHNLPELSALLGLDAVQAKLEEEBOKERAKKQKYNQKMSSE	60
Qy	61	AKRLKTVYTEPYSSWIPQEMAAAGFTYKSGIOCFCCSLTFQAGLTLPTEDKRF	120
Db	61	AKRLKTVYTEPYSSWIPQEMAAAGFTYKSGIOCFCCSLTFQAGLTLPTEDKRF	120
Qy	121	HPDCGLANKDVGNIKYDIRYKYLKSLRGSKGRVQSEEARLASFRMPPYVQGISPCV	180
Db	121	HPDCGLANKDVGNIKYDIRYKYLKSLRGSKGRVQSEEARLASFRMPPYVQGISPCV	180
Qy	181	LSBAGFVFGKQDYOQFSCGGCCGNNESGDDPWKEHAKWPKCEPLRSKSSSEETQYI	240
Db	181	LSBAGFVFGKQDYOQFSCGGCCGNNESGDDPWKEHAKWPKCEPLRSKSSSEETQYI	240
Qy	241	QSYKGVDTTGHFNPNVQRELPMASAYCNDISFAYEELALDSFGKMPRESAVGVALA	300
Db	241	QSYKGVDTTGHFNPNVQRELPMASAYCNDISFAYEELALDSFGKMPRESAVGVALA	300
Qy	301	KAGLFTYTGIDKIVOCFSCGGCLEKMQEGDDPLDHTTCFPCNCFPLQNMKSSAEVTPDLOS	360
Db	301	KAGLFTYTGIDKIVOCFSCGGCLEKMQEGDDPLDHTTCFPCNCFPLQNMKSSAEVTPDLOS	360
Qy	361	RGELECELETTSSSNLEDSIAVGPIVPMAGQEAQWFOBAKQNLNEQLRAAYTSASPRHMS	420

Db	361	RGELECELETTSSSNLEDSIAVGPIVPMAGQEAQWFOBAKQNLNEQLRAAYTSASPRHMS	420
Qy	421	LNDISSDLATHLGCDLSIASGHSKPYQRELVLPYFNGNLSVMCVGEAGSGGTVLL	480
Db	421	LNDISSDLATHLGCDLSIASGHSKPYQRELVLPYFNGNLSVMCVGEAGSGGTVLL	480
Qy	481	KXIAFLMAGGCCPLNRPOLVYLSLSTRDEGLASIIICDQLLEKSGSVTEMCNRIQ	540
Db	481	KXIAFLMAGGCCPLNRPOLVYLSLSTRDEGLASIIICDQLLEKSGSVTEMCNRIQ	540
Qy	541	OLKNOVFLDDYKEICSTPOYIGTLQKHLSTRCLLAVTNRARIPRYETLTIEIK	600
Db	541	OLKNOVFLDDYKEICSTPOYIGTLQKHLSTRCLLAVTNRARIPRYETLTIEIK	600
Qy	601	AFPEYNTVCLLKLKLSHMTLRKPMYFPGKQSLQKQKTEPLPAALCAHWOYPPDS	660
Db	601	AFPEYNTVCLLKLKLSHMTLRKPMYFPGKQSLQKQKTEPLPAALCAHWOYPPDS	660
Qy	661	FDVAVFKSYMERLSLNKATAEILKATVSCGGEALACPFSCCFEFDNDLAEAGVDD	720
Db	661	FDVAVFKSYMERLSLNKATAEILKATVSCGGEALACPFSCCFEFDNDLAEAGVDD	720
Qy	721	EDLTMCLMSKFTAORLPFRPLSPAFQEFLAGKRLIELDSROEHODLGLYHLKOINS	780
Db	721	EDLTMCLMSKFTAORLPFRPLSPAFQEFLAGKRLIELDSROEHODLGLYHLKOINS	780
Qy	781	PMWTSAYNNFLNVVSLSTKAGRTVSHLHLVDNKESENIENDDYKHOPEISLO	840
Db	781	PMWTSAYNNFLNVVSLSTKAGRTVSHLHLVDNKESENIENDDYKHOPEISLO	840
Qy	841	MOLRLGLMOICPAVYSKMSSEHLVLAALKTAQOSNTAAQSPVLOFQSGTTLTGLNT	900
Db	841	MOLRLGLMOICPAVYSKMSSEHLVLAALKTAQOSNTAAQSPVLOFQSGTTLTGLNT	900
Qy	901	QYFEDHESLSLRSIHPIRGNTKSPRAHFSVLTFCPEKSGVPTTIDYASAFEPNNE	960
Db	901	QYFEDHESLSLRSIHPIRGNTKSPRAHFSVLTFCPEKSGVPTTIDYASAFEPNNE	960
Qy	961	ERNLAKEEDNVASYNDQORASPLSGQYKLSPVQYKIPCLAVDVANDIVGQDMLTIL	1020
Db	961	ERNLAKEEDNVASYNDQORASPLSGQYKLSPVQYKIPCLAVDVANDIVGQDMLTIL	1020
Qy	1021	MTVPASQRIELHNSRGITISIRPALELSAASYTKCSISKLELSAAGELLTLPSLE	1080
Db	1021	MTVPASQRIELHNSRGITISIRPALELSAASYTKCSISKLELSAAGELLTLPSLE	1080
Qy	1081	SLVSGTIOGDDOIFRMLDKYCLKEISVDLEGNINVSYPPEPFNHNKXLLIQISA	1140
Db	1081	SLVSGTIOGDDOIFRMLDKYCLKEISVDLEGNINVSYPPEPFNHNKXLLIQISA	1140
Qy	1141	EYDPSKIVKLIQNSPMLVHFHLKCNFSDPGSLMTMLVSGKXLTLSKSDSFGQAVPVA	1200
Db	1141	EYDPSKIVKLIQNSPMLVHFHLKCNFSDPGSLMTMLVSGKXLTLSKSDSFGQAVPVA	1200
Qy	1201	SLRNFISLKLINLEGOQFPDEETSEKFAVILGSLNLELILPTGDDGIYVAKLIIQOCO	1260
Db	1201	SLRNFISLKLINLEGOQFPDEETSEKFAVILGSLNLELILPTGDDGIYVAKLIIQOCO	1260
Qy	1261	QHLCLRLVSFFKTLNDDVVEIKVAISGGFOKLENLKLISNHNKITEGGRNFOALDDM	1320
Db	1261	QHLCLRLVSFFKTLNDDVVEIKVAISGGFOKLENLKLISNHNKITEGGRNFOALDDM	1320
Qy	1321	PNLOELDSRHFTCTCAQATTKYSLSQCVLRPLRLNMLSLDADADIALLVNKKER	1380
Db	1321	PNLOELDSRHFTCTCAQATTKYSLSQCVLRPLRLNMLSLDADADIALLVNKKER	1380
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RESULT 2

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US-08-913-322-24
; Sequence 24, Application US/08913322
; Publication No. US20020137028A1
; GENERAL INFORMATION:
; APPLICANT: Korneiluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Roy, Natalie
; APPLICANT: Robertson, George
; APPLICANT: Tamai, Katsu
; TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INHIBITOR
; FILE REFERENCE: 07891/013001
; CURRENT APPLICATION NUMBER: US/08/913,322
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: PCT/1997/00142
; EARLIER FILING DATE: 1997-01-17
; EARLIER APPLICATION NUMBER: GB 9601108.5
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1403
; TYPE: PRF
; ORGANISM: Homo sapiens
US-08-913-322-24

Query Match      100.0%; Score 1403; DB 8; Length 1403;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATOQKADDERISQFDHNLPELSALGLDAVOLAKELBEEQKEKAKQKYNQMSRSE 60
DB 1 MATOQKADDERISQFDHNLPELSALGLDAVOLAKELBEEQKEKAKQKYNQMSRSE 60
QY 61 AKRLTPTVTPYPERYSWIPQEMAAAGFTFTGYSKGIQCFCSSLLFAGLITRPIEDHRRF 120
DB 61 AKRLTPTVTPYPERYSWIPQEMAAAGFTFTGYSKGIQCFCSSLLFAGLITRPIEDHRRF 120
QY 61 AKRLTPTVTPYPERYSWIPQEMAAAGFTFTGYSKGIQCFCSSLLFAGLITRPIEDHRRF 120
DB 61 AKRLTPTVTPYPERYSWIPQEMAAAGFTFTGYSKGIQCFCSSLLFAGLITRPIEDHRRF 120
QY 121 HPDCCFLINKDVGNIAKYDIRKMLKSRRLGKKRKYQEBEARLASFRMPFYVQGISPCV 180
DB 121 HPDCCFLINKDVGNIAKYDIRKMLKSRRLGKKRKYQEBEARLASFRMPFYVQGISPCV 180
QY 121 HPDCCFLINKDVGNIAKYDIRKMLKSRRLGKKRKYQEBEARLASFRMPFYVQGISPCV 180
DB 121 HPDCCFLINKDVGNIAKYDIRKMLKSRRLGKKRKYQEBEARLASFRMPFYVQGISPCV 180
QY 181 LSEAGFVTTGQDPTVQCSGGCIGNNEBGDDPWKHAHKKFPCGCELRKSKSSEITQYT 240
DB 181 LSEAGFVTTGQDPTVQCSGGCIGNNEBGDDPWKHAHKKFPCGCELRKSKSSEITQYT 240
QY 181 LSEAGFVTTGQDPTVQCSGGCIGNNEBGDDPWKHAHKKFPCGCELRKSKSSEITQYT 240
DB 181 LSEAGFVTTGQDPTVQCSGGCIGNNEBGDDPWKHAHKKFPCGCELRKSKSSEITQYT 240
QY 241 QSYKGFVDITGEHFVNSVQRELPMASAYCNDISIFAYBELRDSFCDMPRESAVGAAALA 300
DB 241 QSYKGFVDITGEHFVNSVQRELPMASAYCNDISIFAYBELRDSFCDMPRESAVGAAALA 300
QY 301 KAGLFYTGIKOIVQFCGCGCLEKWOEGDDPLDHTRCFPNCCFLONMKSAAEVTPIQOS 360
DB 301 KAGLFYTGIKOIVQFCGCGCLEKWOEGDDPLDHTRCFPNCCFLONMKSAAEVTPIQOS 360
QY 301 KAGLFYTGIKOIVQFCGCGCLEKWOEGDDPLDHTRCFPNCCFLONMKSAAEVTPIQOS 360
DB 301 KAGLFYTGIKOIVQFCGCGCLEKWOEGDDPLDHTRCFPNCCFLONMKSAAEVTPIQOS 360
QY 361 RELCELETTSESUJEDSIAVGPIVPEMAQGEAOMFOBAKUNLEOLRAAYTSASFRHMS 420
DB 361 RELCELETTSESUJEDSIAVGPIVPEMAQGEAOMFOBAKUNLEOLRAAYTSASFRHMS 420
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DB 421 LLDISSDLATTHLLJCCDISIASKHSKRPVQSPVLVPEVGNLSVNCVGEAGSKTYVL 480
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DB 541 QKKNQVLLDDYKXICGIPQVIGKLIQKXHLSTCLLIIVTNRNARDIRRLLETILBIK 600
QY 541 QKKNQVLLDDYKXICGIPQVIGKLIQKXHLSTCLLIIVTNRNARDIRRLLETILBIK 600
DB 541 QKKNQVLLDDYKXICGIPQVIGKLIQKXHLSTCLLIIVTNRNARDIRRLLETILBIK 600
QY 601 APPFNTVTCILAKLFSHMTRLARKFNVYFGKQSIQKTIQKTPLFVAALCAHFOYPPDPS 660
DB 601 APPFNTVTCILAKLFSHMTRLARKFNVYFGKQSIQKTIQKTPLFVAALCAHFOYPPDPS 660
QY 601 APPFNTVTCILAKLFSHMTRLARKFNVYFGKQSIQKTIQKTPLFVAALCAHFOYPPDPS 660
DB 601 APPFNTVTCILAKLFSHMTRLARKFNVYFGKQSIQKTIQKTPLFVAALCAHFOYPPDPS 660

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QY 661 FDDVAVFKSYMERLSTBRKATATETATVSSCGELALKGPFSCCFEFPNDLDAEAGVND 720
DB 661 FDDVAVFKSYMERLSTBRKATATETATVSSCGELALKGPFSCCFEFPNDLDAEAGVND 720
QY 721 EDLTWCMSKFTAORLAPRYFLSPAFQELAGRLIETLDSRQEHODLGYHLKOINS 780
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QY 781 PMMTVSANNPLNLYVSSLPSTKAGPKVSHLLHLVNKESLEINSDNYLKHQDEISIQ 840
DB 781 PMMTVSANNPLNLYVSSLPSTKAGPKVSHLLHLVNKESLEINSDNYLKHQDEISIQ 840
QY 841 MOLLRLGWLQICPOAVFSVSEHLLVLAIKTAAYOSNTVAASPEVLQFLOGRTLTGALNL 900
DB 841 MOLLRLGWLQICPOAVFSVSEHLLVLAIKTAAYOSNTVAASPEVLQFLOGRTLTGALNL 900
QY 901 QYFDPHPSISILNLSIHPPITGKNTSFRARFVLETCFQKSGYPTIDQYASAEFPNNEW 960
DB 901 QYFDPHPSISILNLSIHPPITGKNTSFRARFVLETCFQKSGYPTIDQYASAEFPNNEW 960
QY 961 EBNLAEKEDNVKSYNDQMRASPDLSGYKLSPKQYKIPCLEVDVNDIDVVGOMLTEL 1020
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QY 1141 EYDPSKVLKLIQNSBNLAVHLLKCNFSDSGSLMTMLVSCKLTETKESDSFOAVPVA 1200
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QY 1201 SLNPFISLKLINLGGQFPDEETSEKFAVILGSLNMLELILPTGDIQIRVAKLLIOQCO 1260
DB 1201 SLNPFISLKLINLGGQFPDEETSEKFAVILGSLNMLELILPTGDIQIRVAKLLIOQCO 1260
QY 1261 QHCHLRVLSPEKTLNDSVYELIAVAISGFQCLBNLKLSINHKTITEEGRFPQALNM 1320
DB 1261 QHCHLRVLSPEKTLNDSVYELIAVAISGFQCLBNLKLSINHKTITEEGRFPQALNM 1320
QY 1321 PMLQELDISRHFTECIRAOATTVKSSQCVLRPLRILNMLSWLIDADDIALVNMER 1380
DB 1321 PMLQELDISRHFTECIRAOATTVKSSQCVLRPLRILNMLSWLIDADDIALVNMER 1380
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DB 1381 HPQSKTYLTLLQKWLPPSPRIIOK 1403

RESULT 3
US-10-285-408-1
; Sequence 1, Application US/10285408
; Publication No. US20030108967A1
; GENERAL INFORMATION:
; APPLICANT: IKEDA, Johe
; APPLICANT: SAKAI, Harumi
; TITLE OF INVENTION: Monoclonal Antibodies Against Human Apoptosis Inhibitory Protein
; FILE REFERENCE: 2002-1440/MMC/00653
; CURRENT APPLICATION NUMBER: US/10/285,408
; EARLIER FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/830,338
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: PCT/JP99/05841
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 1403

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TYPE: PR1
ORGANISM: Homo sapiens
us-10-285-408-1

Query Match 100.0%; Score 1403; DB 15; Length 1403;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MATQKASDERISQFDNLILPELSALLGLDAVOLAKELSEEEQEKRAKQKYNQNRSE 60
DB 1 MATQKASDERISQFDNLILPELSALLGLDAVOLAKELSEEEQEKRAKQKYNQNRSE 60
QY 61 AKRLKTYTEPYSSNIPOEMAAAGFTYVGSQIOCFCSLLIAGLITLPIEDHKRP 120
DB 61 AKRLKTYTEPYSSNIPOEMAAAGFTYVGSQIOCFCSLLIAGLITLPIEDHKRP 120
QY 121 HPDGFLLNKDVGNIAKYDIRVKNLKSRLGCMRYQEEEARLAFRNMPFYVQGISPCV 180
DB 121 HPDGFLLNKDVGNIAKYDIRVKNLKSRLGCMRYQEEEARLAFRNMPFYVQGISPCV 180
QY 181 LSAGVFTGKODTYQCFSCGCGIAGWEGDDPWKEHAKMFKCEFLRSKSGSEETIOTI 240
DB 181 LSAGVFTGKODTYQCFSCGCGIAGWEGDDPWKEHAKMFKCEFLRSKSGSEETIOTI 240
QY 241 QSYKGFVDITGBHPNVMQBELPMASAYCNDISIPAYEBELRDSFKDMPRESVGVAAIA 300
DB 241 QSYKGFVDITGBHPNVMQBELPMASAYCNDISIPAYEBELRDSFKDMPRESVGVAAIA 300
QY 301 KAGLFYTGIKDIYVCFSCGCGIEMQEGDDPLDHTRCFPCNCFLONMKSSAEVTPDIQS 360
DB 301 KAGLFYTGIKDIYVCFSCGCGIEMQEGDDPLDHTRCFPCNCFLONMKSSAEVTPDIQS 360
QY 361 RGEICELLETSSSNLEDSIAVPIVPMAGSEOMFOENKUNLEQLAAATYSAPFRHMS 420
DB 361 RGEICELLETSSSNLEDSIAVPIVPMAGSEOMFOENKUNLEQLAAATYSAPFRHMS 420
QY 421 LLDISSDLATDHLGCDLSIASKISKVEEPLVLEVFNGINSVMCEGASGKTVLL 480
DB 421 LLDISSDLATDHLGCDLSIASKISKVEEPLVLEVFNGINSVMCEGASGKTVLL 480
QY 481 KKIAPLWAGCCPLNRPQVLFVLSLSSTRPDEGLASIIICOLLEKSGSTBEMCANIIO 540
DB 481 KKIAPLWAGCCPLNRPQVLFVLSLSSTRPDEGLASIIICOLLEKSGSTBEMCANIIO 540
QY 541 QLNQCVLFLDDYKESISIPVIGKLIQXNHLSTRCLIAVTRRADIRRYLETILBIX 600
DB 541 QLNQCVLFLDDYKESISIPVIGKLIQXNHLSTRCLIAVTRRADIRRYLETILBIX 600
QY 601 APPFNVTGCIIRKLFSHNMTLRKFWYFGKQSIQKIQCTPFVAALCAHMFQYFDPDS 660
DB 601 APPFNVTGCIIRKLFSHNMTLRKFWYFGKQSIQKIQCTPFVAALCAHMFQYFDPDS 660
QY 661 FDDVAVFESYMERLSIRNKATAEILKATVSCGELAKGFSCCFEFNDLDAEAGDED 720
DB 661 FDDVAVFESYMERLSIRNKATAEILKATVSCGELAKGFSCCFEFNDLDAEAGDED 720
QY 721 EDLTMCLMSKFTQORARPFRFLSPAFOEFLAQRILIELLSDROEHODGLYHLKQINS 780
DB 721 EDLTMCLMSKFTQORARPFRFLSPAFOEFLAQRILIELLSDROEHODGLYHLKQINS 780
QY 781 PMMTVAANNPLNVSLSIPSTRKAPKIVSHLHLVONKESLENISENDVYLKIQEPISIQ 840
DB 781 PMMTVAANNPLNVSLSIPSTRKAPKIVSHLHLVONKESLENISENDVYLKIQEPISIQ 840
QY 841 MOLLRLAOTICQAVFSNVSEHLVIALKTAQVSTVAAAGPPYLGTLQGRITLIGALNL 900
DB 841 MOLLRLAOTICQAVFSNVSEHLVIALKTAQVSTVAAAGPPYLGTLQGRITLIGALNL 900
QY 901 QYFPHPSLSILRSIHPIRGNKTSPPRAHPSVLETGCDKSOVPTIDODYASAFENMEM 960
DB 901 QYFPHPSLSILRSIHPIRGNKTSPPRAHPSVLETGCDKSOVPTIDODYASAFENMEM 960
QY 961 EBNLAEKEDNVKSYMQRASPDISTGYKLSFKQYKIPCELVNDVIDVGGOMLEIL 1020

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DB 961 EBNLAEKEDNVKSYMQRASPDISTGYKLSFKQYKIPCELVNDVIDVGGOMLEIL 1020
QY 1021 MTFVPSASRIEILHNHGRPIESIRPALELSKASVTCSSIKLELSAABOELLITLPSLE 1080
DB 1021 MTFVPSASRIEILHNHGRPIESIRPALELSKASVTCSSIKLELSAABOELLITLPSLE 1080
QY 1081 SLEWSTGTSQODQIFPNLDKFLCLKELSVDLEGININFSYIPBEPNPFHNEKLIQISA 1140
DB 1081 SLEWSTGTSQODQIFPNLDKFLCLKELSVDLEGININFSYIPBEPNPFHNEKLIQISA 1140
QY 1141 EYDPSKLVKLIQNSPULHAFHLKCNFFSDGSLMTWLVSCKLJTEIKFSDSPQAVPVA 1200
DB 1141 EYDPSKLVKLIQNSPULHAFHLKCNFFSDGSLMTWLVSCKLJTEIKFSDSPQAVPVA 1200
QY 1201 SLPNFTSLKILNLEQOPDEETSEKPAVILGSLNLEBILIPGOGIYVAKLIIOQCO 1260
DB 1201 SLPNFTSLKILNLEQOPDEETSEKPAVILGSLNLEBILIPGOGIYVAKLIIOQCO 1260
QY 1261 QLMCLAVTSFFPTLINDSVVEIAKVAISGGFOKLENLKLSINHKITEGYNFPQALDNM 1320
DB 1261 QLMCLAVTSFFPTLINDSVVEIAKVAISGGFOKLENLKLSINHKITEGYNFPQALDNM 1320
QY 1321 PNLQELDISRHFTCEICAKAOTYKLSISOCVLRPLRLNMLSMULDADDIALNVMKER 1380
DB 1321 PNLQELDISRHFTCEICAKAOTYKLSISOCVLRPLRLNMLSMULDADDIALNVMKER 1380
QY 1381 HPOSKYLTILQKWLIFSPHIIQK 1403
DB 1381 HPOSKYLTILQKWLIFSPHIIQK 1403

```

RESULT 4
US-09-841-739-9
Sequence 9, Application US/09841739
Patent No. US20020034784A1
GENERAL INFORMATION:
APPLICANT: Bactin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-329001
CURRENT APPLICATION NUMBER: US/09-841, 739
PRIOR FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 782
TYPE: PR1
ORGANISM: Homo sapiens
US-09-841-739-9

Query Match 35.4%; Score 496; DB 9; Length 782;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 451 EPLVLEPVEFGNINSVMCEVGEAGSGKTVLLKKIAPLWAGCCPLNRPQVLFVLSSTR 510
DB 1 EPLVLEPVEFGNINSVMCEVGEAGSGKTVLLKKIAPLWAGCCPLNRPQVLFVLSSTR 510
QY 511 PDEGLASIIICOLLLEKSGSTBEMCANIIOQLKQCVLFLDDYKESISIPVIGKLIQXN 60
DB 61 PDEGLASIIICOLLLEKSGSTBEMCANIIOQLKQCVLFLDDYKESISIPVIGKLIQXN 60
QY 571 HHSRTCLIAVTRRADIRRYLETILBIXKAPFYNTVTCIRLFSHNMTLRKRWYFG 630
DB 571 HHSRTCLIAVTRRADIRRYLETILBIXKAPFYNTVTCIRLFSHNMTLRKRWYFG 630
QY 121 HHSRTCLIAVTRRADIRRYLETILBIXKAPFYNTVTCIRLFSHNMTLRKRWYFG 180
DB 121 HHSRTCLIAVTRRADIRRYLETILBIXKAPFYNTVTCIRLFSHNMTLRKRWYFG 180
QY 631 KQOSLOKIQCTPFVAALCAHMFQYFDPDSFDDVAVFESYMERLSIRNKATAEILKATV 690
DB 631 KQOSLOKIQCTPFVAALCAHMFQYFDPDSFDDVAVFESYMERLSIRNKATAEILKATV 690

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QY 691 SCGEALAGFSSCCFEFNDDDLAAGVDEDEDLTMCLMSKFTNORLRPPYRFLSPAFQOF 750
DB 241 SCGEALAGFSSCCFEFNDDDLAAGVDEDEDLTMCLMSKFTNORLRPPYRFLSPAFQOF 306
QY 751 LAGMRLIELLSDRQEHODLGLVHLKQINSMMTVSANNFLNYSLSLSTAGPKIVSH 810
DB 301 LAGMRLIELLSDRQEHODLGLVHLKQINSMMTVSANNFLNYSLSLSTAGPKIVSH 360
QY 811 LHLVDNKSLENISENDYDLKHOPETSLQMLRGIMQICQAFYSWSEHLVLAJKT 870
DB 361 LHLVDNKSLENISENDYDLKHOPETSLQMLRGIMQICQAFYSWSEHLVLAJKT 420
QY 871 AVQSTVAACSPFVLOFLOGRTLTGALNLQYFFDHPBSLSLRSHIFIRGNKTSPPAH 930
DB 421 AVQSTVAACSPFVLOFLOGRTLTGALNLQYFFDHPBSLSLRSHIFIRGNKTSPPAH 480
QY 931 FSVLETCFDSKQVFTIIDDYASAFEPNNWERMLAEKEDNVSYNDMQRASPDISTGYM 990
DB 481 FSVLETCFDSKQVFTIIDDYASAFEPNNWERMLAEKEDNVSYNDMQRASPDISTGYM 540
QY 991 KLSPKQYKIPCLLEVVDNDIVVGODMLEILMTVFSASQRIELHLSRGFISIRPAEL 1050
DB 541 KLSPKQYKIPCLLEVVDNDIVVGODMLEILMTVFSASQRIELHLSRGFISIRPAEL 600
QY 1051 SKASTYKCSISKLELSAAEOELTLTPSLSELEVSCTIOSQOQIFPNLDKFLCKELSV 1110
DB 601 SKASTYKCSISKLELSAAEOELTLTPSLSELEVSCTIOSQOQIFPNLDKFLCKELSV 660
QY 1111 LEGNINVSVIPPEFPNFMHEKLLIQISAEDPSKLV 1148
DB 661 LEGNINVSVIPPEFPNFMHEKLLIQISAEDPSKLV 698

```

RESULT 5
US-10-449-315-9

```

; Sequence 9, Application US/10449315
; Publication No. US20030190679A1
; GENERAL INFORMATION:
; APPLICANT: Berth, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 0734-432901
; CURRENT APPLICATION NUMBER: US/10/449,315
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 782
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-315-9

```

Query Match 35.4%; Score 496; DB 12; Length 782;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 451 EPLVPEVFGNLSVMEVGEAGSGKTVLAKKIAPLWASGCCPLNRPOLVYLSLSSTR 510
DB 1 EPLVPEVFGNLSVMEVGEAGSGKTVLAKKIAPLWASGCCPLNRPOLVYLSLSSTR 60
QY 511 PREGIASIICQQLLEKSGSTVMCMRNITIOQLKXQVFLLDYKEICSIPOYIGLIXN 570
DB 61 PREGIASIICQQLLEKSGSTVMCMRNITIOQLKXQVFLLDYKEICSIPOYIGLIXN 120
QY 571 HLSRTCLIAVTRNARDIRRYETLIEIKAPFPYTVCLRLKLFSHNTRLRKEMVYFG 630
DB 121 HLSRTCLIAVTRNARDIRRYETLIEIKAPFPYTVCLRLKLFSHNTRLRKEMVYFG 180

```

```

QY 631 KNQSIQKIQKPLFVAAI CAHWFOYFPDPSFDVANFASMYERLSLRNKATREILKATVS 690
DB 181 KNQSIQKIQKPLFVAAI CAHWFOYFPDPSFDVANFASMYERLSLRNKATREILKATVS 240
QY 691 SCGEALAGFSSCCFEFNDDDLAAGVDEDEDLTMCLMSKFTNORLRPPYRFLSPAFQOF 750
DB 241 SCGEALAGFSSCCFEFNDDDLAAGVDEDEDLTMCLMSKFTNORLRPPYRFLSPAFQOF 300
QY 751 LAGMRLIELLSDRQEHODLGLVHLKQINSMMTVSANNFLNYSLSLSTAGPKIVSH 810
DB 301 LAGMRLIELLSDRQEHODLGLVHLKQINSMMTVSANNFLNYSLSLSTAGPKIVSH 360
QY 811 LHLVDNKSLENISENDYDLKHOPETSLQMLRGIMQICQAFYSWSEHLVLAJKT 870
DB 361 LHLVDNKSLENISENDYDLKHOPETSLQMLRGIMQICQAFYSWSEHLVLAJKT 420
QY 871 AVQSTVAACSPFVLOFLOGRTLTGALNLQYFFDHPBSLSLRSHIFIRGNKTSPPAH 930
DB 421 AVQSTVAACSPFVLOFLOGRTLTGALNLQYFFDHPBSLSLRSHIFIRGNKTSPPAH 480
QY 931 FSVLETCFDSKQVFTIIDDYASAFEPNNWERMLAEKEDNVSYNDMQRASPDISTGYM 990
DB 481 FSVLETCFDSKQVFTIIDDYASAFEPNNWERMLAEKEDNVSYNDMQRASPDISTGYM 540
QY 991 KLSPKQYKIPCLLEVVDNDIVVGODMLEILMTVFSASQRIELHLSRGFISIRPAEL 1050
DB 541 KLSPKQYKIPCLLEVVDNDIVVGODMLEILMTVFSASQRIELHLSRGFISIRPAEL 600
QY 1051 SKASTYKCSISKLELSAAEOELTLTPSLSELEVSCTIOSQOQIFPNLDKFLCKELSV 1110
DB 601 SKASTYKCSISKLELSAAEOELTLTPSLSELEVSCTIOSQOQIFPNLDKFLCKELSV 660
QY 1111 LEGNINVSVIPPEFPNFMHEKLLIQISAEDPSKLV 1148
DB 661 LEGNINVSVIPPEFPNFMHEKLLIQISAEDPSKLV 698

```

RESULT 6
US-10-029-386-33707

```

; Sequence 33707, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENEOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33707
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO U80017.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.91
; OTHER INFORMATION: SWISSPROT HIT: Q13075, EVALU0 0.00e+00
US-10-029-386-33707

```

Query Match 27.4%; Score 385; DB 12; Length 385;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 707 FVDDDLAAGVDEDEDLTMCLMSKFTNORLRPPYRFLSPAFQFLAGMRLIELLSDRQEH 766
DB 1 FVDDDLAAGVDEDEDLTMCLMSKFTNORLRPPYRFLSPAFQFLAGMRLIELLSDRQEH 60
QY 767 HODGLVHLKQINSMMTVSANNFLNYSLSLSTAGPKIVSHLHLVDNKSLENISE 826

```

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Db      61  HDLGLYHLKQINSPMTVSAVNNFLVYSSLESTAGKIVSHLHLVDNKESLENISE 120
Qy      827  NDDYLGHQPEISLQWOLRGMOJCQAYFSVMSSEHLVLTALKTAQVQSTVAACSPPVLO 886
Db      121  NDDYLGHQPEISLQWOLRGMOJCQAYFSVMSSEHLVLTALKTAQVQSTVAACSPPVLO 180
Qy      887  FLOGRTLTGALNLYQFPDHEESLSLRSHFPIKQNTKSPRAHPSVLETCFQKQVPTI 946
Db      181  FLOGRTLTGALNLYQFPDHEESLSLRSHFPIKQNTKSPRAHPSVLETCFQKQVPTI 240
Qy      947  DDDVSAFEPNMEWERNLAKEEDNVKSYMDQRRASPLSTGYKLSPPQYKIPCLEVDV 1006
Db      241  DDDVSAFEPNMEWERNLAKEEDNVKSYMDQRRASPLSTGYKLSPPQYKIPCLEVDV 300
Qy      1007  NDIDVAGQDMLEIMTYFASQRIEHLNHSRGTIESIRPALAISKASVTKCSISKLELS 1066
Db      301  NDIDVAGQDMLEIMTYFASQRIEHLNHSRGTIESIRPALAISKASVTKCSISKLELS 360
Qy      1067  AAQBELLTTPSLSELEVSCTTOSQ 1091
Db      361  AAQBELLTTPSLSELEVSCTTOSQ 385

```

RESULT 7

```

US-10-029-386-33933
/ Sequence 33933, Application US/10029386
/ Publication No. US20030194704A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David K.
/ APPLICANT: Hanzel, David K.
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
/ FILE REFERENCE: AEWICA-X-2
/ CURRENT APPLICATION NUMBER: US/10/029,386
/ NUMBER OF SEQ ID NOS: 2001-13-20
/ SOFTWARE: Annotmax Sequence Mapping Engine vers. 1.1
/ SEQ ID NO 33933
/ LENGTH: 203
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC005031.1
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.95
/ OTHER INFORMATION: SWISSPROT HIT: Q13075, EVALUATE 1.00e-112
US-10-029-386-33933

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Query Match
Best Local Similarity 14.5%; Score 203; DB 12; Length 203;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      389  MAQGEAQMFOEAKNLEQULRAAYTSASFRHMSLDDISSDLATTHLGCGLSTASRHISKP 448
Db      1  MAQGEAQMFOEAKNLEQULRAAYTSASFRHMSLDDISSDLATTHLGCGLSTASRHISKP 60
Qy      449  VOEFVLVPEVFGLNSVWCVGEAGSGKTIVLKKIAFLWASGCCPLNRFQVLYLSS 508
Db      61  VOEFVLVPEVFGLNSVWCVGEAGSGKTIVLKKIAFLWASGCCPLNRFQVLYLSS 120
Qy      509  TRDEGLASTICDQULEKSGSVTEKCRNIIQOLKNQVFLDDYKKEICSIPOVIGLQ 568
Db      121  TRDEGLASTICDQULEKSGSVTEKCRNIIQOLKNQVFLDDYKKEICSIPOVIGLQ 180
Qy      569  KNLHSTCLLIIVATNRARDIR 591
Db      181  KNLHSTCLLIIVATNRARDIR 203

```

RESULT 8
US-09-925-299-1033
/ Sequence 1033, Application US/09925299

```

/ Patent No. US20020055627A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: PA102
/ CURRENT APPLICATION NUMBER: US/09/925,299
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05883
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: 60/124,270
/ NUMBER OF SEQ ID NOS: 1556
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1033
/ LENGTH: 118
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-925-299-1033

```

Query Match
Best Local Similarity 5.3%; Score 75; DB 9; Length 118;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      607  TVCILRLKLFSSNMTRLRKEMVYFGKQNSLOKIQKTPLFVAALCAHMFQYPPDPSFDDVAV 666
Db      1  TVCILRLKLFSSNMTRLRKEMVYFGKQNSLOKIQKTPLFVAALCAHMFQYPPDPSFDDVAV 60
Qy      667  FKSVMERLSLNKAT 681
Db      61  FKSVMERLSLNKAT 75

```

RESULT 9

```

US-09-925-299-1033
/ Sequence 1033, Application US/09925299
/ Publication No. US20030040617A9
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: PA102
/ CURRENT APPLICATION NUMBER: US/09/925,299
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05883
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: 60/124,270
/ NUMBER OF SEQ ID NOS: 1556
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1033
/ LENGTH: 118
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-925-299-1033

```

Query Match
Best Local Similarity 5.3%; Score 75; DB 11; Length 118;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      607  TVCILRLKLFSSNMTRLRKEMVYFGKQNSLOKIQKTPLFVAALCAHMFQYPPDPSFDDVAV 666
Db      1  TVCILRLKLFSSNMTRLRKEMVYFGKQNSLOKIQKTPLFVAALCAHMFQYPPDPSFDDVAV 60
Qy      667  FKSVMERLSLNKAT 681
Db      61  FKSVMERLSLNKAT 75

```

RESULT 10
US-10-138-618-26
/ Sequence 26, Application US/10138618
/ Publication No. US20030100525A1
/ GENERAL INFORMATION:
/ APPLICANT: Altieri, Dario C.

TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-138-618-26
Query Match 3.6%; Score 50; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 6.5e-40;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 306 YTGIDIVQCFSCGCGCLEKWEQGGDPLDHTRCFPNCPFLQNNKSSAAYT 355
DB 1 YTGIDIVQCFSCGCGCLEKWEQGGDPLDHTRCFPNCPFLQNNKSSAAYT 50
RESULT 11
US-10-138-618-13
Sequence 13, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-138-618-13
Query Match 3.3%; Score 47; DB 15; Length 47;
Best Local Similarity 100.0%; Pred. No. 4.8e-37;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 159 BEARLASFRNMPFYVGISPCVLSBAGFVFTGKQDTVQCFSCGCGCIG 205
DB 1 BEARLASFRNMPFYVGISPCVLSBAGFVFTGKQDTVQCFSCGCGCIG 47
RESULT 12
US-09-864-761-47337
Sequence 47337, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,667
; PRIOR FILING DATE: 2000-09-23
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-10
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47337
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005031.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.53
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.55
; OTHER INFORMATION: SWISSPROT HIT: Q13075, EVALU8 5.00e-06
; US-09-864-761-67337

Query Match
Best Local Similarity 1.6%; Score 22; DB 9; Length 37;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 SKKSEETQYIOGYKGFVDIT 250
Db 1 SKKSEETQYIOGYKGFVDIT 22

RESULT 13
US-09-841-739-11
; Sequence 11, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 0734-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: majority sequence
; US-09-841-739-11

Query Match
Best Local Similarity 0.9%; Score 12; DB 9; Length 898;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 639 OKTPELVAAICA 650
Db 193 OKTPELVAAICA 204

RESULT 14
US-10-449-315-11
; Sequence 11, Application US/10449315
; Publication No. US20030190679A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
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; FILE REFERENCE: 0734-329001
; CURRENT APPLICATION NUMBER: US/10/449,315
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: majority sequence
; US-10-449-315-11

Query Match
Best Local Similarity 0.9%; Score 12; DB 12; Length 898;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 639 OKTPELVAAICA 650
Db 193 OKTPELVAAICA 204

RESULT 15
US-09-812-471-20
; Sequence 20, Application US/09812471
; Patent No. US20020018765A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/062002
; CURRENT APPLICATION NUMBER: US/09/812,471
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: US 60/216,723
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: derived from Polyoma virus large T antigen
; US-09-812-471-20

Query Match
Best Local Similarity 0.6%; Score 8; DB 9; Length 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 326 QEGDDPLD 333
Db 3 QEGDDPLD 10

RESULT 16
US-09-812-633-20
; Sequence 20, Application US/09812633
; Patent No. US20020147996A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; APPLICANT: Li, Dawei
; APPLICANT: Mok, Samuel C.
; APPLICANT: Cramer, Daniel W.
; APPLICANT: Ma, Yupo
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/066001
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; CURRENT APPLICATION NUMBER: US/09/812,633
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: US 60/216,723
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: derived from Polyoma virus large T antigen
US-09-812-633-20

Query Match
Best Local Similarity 100.0%; Score 8; DB 10; Length 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPLD 333
Db 3 QEGDDPLD 10

RESULT 17
US-09-988-117-20
; Sequence 20, Application US/09988117
; Patent No. US20020156039A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; APPLICANT: Li, Dawei
; APPLICANT: Mok, Samuel C.
; APPLICANT: Cramer, Daniel W.
; APPLICANT: Ma, Yupo
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/066002
; CURRENT APPLICATION NUMBER: US/09/988,117
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/812,633
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: US 60/216,723
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: derived from Polyoma virus large T antigen
US-09-988-117-20

Query Match
Best Local Similarity 100.0%; Score 8; DB 10; Length 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPLD 333
Db 3 QEGDDPLD 10

RESULT 18
US-09-933-767-580
; Sequence 580, Application US/09933767
; Publication No. US2003018192A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US96/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,971
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,883
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,897
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,898
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,962

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;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,963
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,877
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,878
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/068,054
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,064
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,053
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/070,923
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/073,160
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/073,159
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/073,165
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/073,164
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/085,925
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,921
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,923
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,922
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/092,921
;; PRIOR FILING DATE: 1998-07-15
;; PRIOR APPLICATION NUMBER: 60/094,657
;; NUMBER OF SEQ ID NOS: 1245
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 580
;; LENGTH: 64
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-933-767-580

Query Match 0.64; Score 8; DB 12; Length 64;
Best Local Similarity 100.0%; Pred No 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 39 EEEEXKER 46
DB 29 EEEEXKER 36

RESULT 19
US-10-023-282-580
;; Sequence 580: Application US/10023282
;; Publication No. US2003092893A1
;; GENERAL INFORMATION:
;; APPLICANT: Young et al.
;; TITLE OF INVENTION: 207 Human Secreted Proteins
;; FILE REFERENCE: P2007P1
;; CURRENT APPLICATION NUMBER: US/10/023,282
;; EARLIER FILING DATE: 2001-12-20
;; EARLIER APPLICATION NUMBER: 09/205,258
;; EARLIER FILING DATE: 1998-12-04
;; EARLIER APPLICATION NUMBER: 09/205,258
;; EARLIER FILING DATE: 1998-06-04
;; EARLIER APPLICATION NUMBER: 60/048,885
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,375
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,881
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,880

;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,896
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,020
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,876
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,895
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,884
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,894
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,971
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,964
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,882
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,899
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,893
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,900
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,901
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,892
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,915
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,019
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,970
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,972
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,916
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,373
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,875
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,374
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,917
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,949
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,974
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,883
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,897
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,898
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,962
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,963
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,877
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,878
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/070,923
;; EARLIER FILING DATE: 1997-12-18
;; EARLIER APPLICATION NUMBER: 60/092,921
;; EARLIER FILING DATE: 1998-07-15
;; EARLIER APPLICATION NUMBER: 60/094,657
;; NUMBER OF SEQ ID NOS: 1227
;; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 580
LENGTH: 64
TYPE: PRT
ORGANISM: Homo sapiens
US-10-023-282-580

Query Match
Best Local Similarity 100.0%; DB 15; Length 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEOKER 46
Db 29 EEEOKER 36

RESULT 20
US-09-201-936-16
Sequence 16, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003003
CURRENT FILING DATE: US/09/201,936
EARLIER FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 68
TYPE: PRT
ORGANISM: Mus musculus
US-09-201-936-16

Query Match
Best Local Similarity 100.0%; DB 10; Length 68;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 DTVOCFSC 200
Db 34 DTVOCFSC 41

RESULT 21
US-09-925-297-743
Sequence 743, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT FILING DATE: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 743
LENGTH: 95
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: 1/4
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-743

Query Match
Best Local Similarity 100.0%; DB 9; Length 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 EKLIIQIS 1139
Db 37 EKLIIQIS 44

RESULT 22
US-10-156-761-8837
Sequence 8837, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8837
LENGTH: 201
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-8837

Query Match
Best Local Similarity 100.0%; DB 15; Length 201;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 SAEVTPDL 358
Db 33 SAEVTPDL 40

RESULT 23
US-09-925-299-821
Sequence 821, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT FILING DATE: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 821
LENGTH: 259
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-299-821

Query Match 0.6%; Score 8; DB 9; Length 259;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 39 EEEEOKKER 46
 DB 174 EEEEOKKER 181

RESULT 24
 US-09-925-299-821
 ; Sequence 821, Application US/09925299
 ; Publication No. US20030040617A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA102
 ; CURRENT APPLICATION NUMBER: US/09/925,299
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05883
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; NUMBER OF SEQ ID NOS: 1556
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 821
 ; LENGTH: 259
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-925-299-821

Query Match 0.6%; Score 8; DB 11; Length 259;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 39 EEEEOKKER 46
 DB 174 EEEEOKKER 181

RESULT 25
 US-10-156-761-12012
 ; Sequence 12012, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; PRIOR FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 12012
 ; LENGTH: 481
 ; TYPE: PRT
 ; ORGANISM: Streptomyces avermitilis
 US-10-156-761-12012

Query Match 0.6%; Score 8; DB 15; Length 481;
 Best Local Similarity 100.0%; Pred. No. 1,3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 293 AVGVAAAL 300

DB 9 AVGVAAAL 16

RESULT 26
 US-09-974-592-10
 ; Sequence 10, Application US/09974592
 ; Patent No. US20020120121A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G
 ; APPLICANT: Mackenzie, Alexander E
 ; APPLICANT: Liston, Peter
 ; APPLICANT: Baird, Stephen
 ; APPLICANT: Tsang, Benjamin K
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 ; FILE REFERENCE: 07891/009004
 ; CURRENT APPLICATION NUMBER: US/09/974,592
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: US 09/617,053
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 08/800,929
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 496
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-974-592-10

Query Match 0.6%; Score 8; DB 10; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1,3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 193 DTVOCFSC 200
 DB 59 DTVOCFSC 66

RESULT 27
 US-09-201-936-10
 ; Sequence 10, Application US/09201936
 ; Publication No. US20020187946A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korneluk, Robert G
 ; APPLICANT: Mackenzie, Alexander E
 ; APPLICANT: Liston, Peter
 ; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 ; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 ; FILE REFERENCE: 07891/003003
 ; CURRENT APPLICATION NUMBER: US/09/201,936
 ; PRIOR FILING DATE: 1998-12-01
 ; PRIOR APPLICATION NUMBER: 09/011,356
 ; PRIOR FILING DATE: 1998-02-04
 ; PRIOR APPLICATION NUMBER: PCT/IB96/01022
 ; PRIOR FILING DATE: 1996-08-05
 ; PRIOR APPLICATION NUMBER: 08/576,956
 ; EARLIER FILING DATE: 1995-12-22
 ; EARLIER APPLICATION NUMBER: 08/511,485
 ; EARLIER FILING DATE: 1995-08-04
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 496
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-201-936-10

Query Match 0.6%; Score 8; DB 10; Length 496;
 US-09-201-936-10

Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 DTVOFCSC 200
|||||
DB 59 DTVOFCSC 66

RESULT 28

US-09-933-767-573
; Sequence 573, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,886
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,971
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916

; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,883
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,897
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,898
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,862
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 573
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (409)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-933-767-573

Query Match 0.6%; Score 8; DB 12; Length 567;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEEXKER 46
|||||

DB 483 EEBOKER 490

RESULT 39
US-10-023-282-573
Sequence 573, Application US/10023282
Publication No. US20030092893A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/10/023, 282
EARLIER FILING DATE: 2001-12-20
EARLIER APPLICATION NUMBER: 09/205, 258
EARLIER FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048, 885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049, 375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049, 020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049, 019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049, 373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049, 374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 949
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048, 974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070, 923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092, 921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094, 657
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 573
LENGTH: 567
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: SITE
NAME/KEY: SITE
LOCATION: (409)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-023-282-573

Query Match 0.64; Score 8; DB 15; Length 567;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 483 EEBOKER 490

RESULT 30
US-09-896-852-55
Sequence 55, Application US/09896852
Patent No. US2002025542A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Maine, Gregory T.
APPLICANT: Hunt, Jeffery C.
APPLICANT: Brojanc, Susan
APPLICANT: Jhy-Tsing, Shue, Michael
APPLICANT: Chovan, Linda E.
APPLICANT: Tyner, Joan D.
TITLE OF INVENTION: ANTIGEN COCKTAILS, P35, AND USES THEREOF
FILE REFERENCE: 6361 US, D1
CURRENT APPLICATION NUMBER: US/09/896, 852
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/086, 503
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 667
TYPE: PRT
ORGANISM: Tokoplasma gondii
US-09-896-852-55

Query Match 0.64; Score 8; DB 9; Length 667;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FGAGITRL 112
DB 542 FGAGITRL 549

RESULT 31

US-09-728-644-55
Sequence 55, Application US/09728644
Publication No. US20030119053A1
GENERAL INFORMATION:
APPLICANT: MAINE, Gregory T.
APPLICANT: HUNT, Jeffrey C.
APPLICANT: BROJANAC, Susan
APPLICANT: JYH-TSING SHEU, Michael
APPLICANT: CHOYAN, Linda E.
APPLICANT: TYNER, Joan D.
APPLICANT: HOWARD, Lawrence V.
APPLICANT: PARMLEY, Stephen F.
APPLICANT: REMINGTON, Jack S.
APPLICANT: ARAUJO, Fausto
APPLICANT: SUZUKI, Yashuhiro
APPLICANT: LI, Shuli
TITLE OF INVENTION: ANTIGEN COCKTAILS, P35 AND USES THEREOF
FILE REFERENCE: 6361.US.P1
CURRENT APPLICATION NUMBER: US/09/728,644
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/303,064
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatsSeq for Windows Version 3.0
SEQ ID NO: 55
LENGTH: 667
TYPE: PRT
ORGANISM: Toxoplasma gondii
US-09-728-644-55

Query Match
Best Local Similarity 100.0%; Score 8; DB 11; Length 667;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FGAGITRL 112
DB 542 FGAGITRL 549

RESULT 32

US-09-968-528-2
Sequence 2, Application US/09969528
Patent No. US20020150567A1
GENERAL INFORMATION:
APPLICANT: POT, David A.
APPLICANT: WILLIAMS, Lewis T.
APPLICANT: JEFFERSON, Anne Bennett
APPLICANT: MEJERUS, Philip W.
TITLE OF INVENTION: NO. US20020150567A1 Gdb2 Associating Protein and Nucleic
Acids Encoding Therefor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,528
FILING DATE: 01-Oct-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/560,005
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-0624000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 976 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match
Best Local Similarity 100.0%; Score 8; DB 10; Length 976;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1075 TLPSLESL 1082
DB 14 TLPSLESL 21

RESULT 33

US-10-291-607-15
Sequence 15, Application US/10291607
Publication No. US20030143232A1
GENERAL INFORMATION:
APPLICANT: ALTIERI, Dario C.
TITLE OF INVENTION: Methods for Selectively Modulating Survivin Apoptosis
FILE REFERENCE: 44574-5063-US
CURRENT APPLICATION NUMBER: US/10/291,607
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US/09/515,514
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 15
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: NAIP phosphorylation motif
US-10-291-607-15

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 WIPQEMA 82
DB 1 WIPQEMA 7

RESULT 34

US-09-812-471-15
Sequence 15, Application US/09812471
Patent No. US20020018765A1
GENERAL INFORMATION:
APPLICANT: BENJAMIN, Thomas L.
TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
FILE REFERENCE: 00742/062002
CURRENT APPLICATION NUMBER: US/09/812,471
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: US 60/216,723

```

; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: derived from Polyoma virus large T antigen
US-09-812-471-15
```

```

Query Match          0.5%; Score 7; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy          326 QEGDDPL 332
Db          3 QEGDDPL 9
```

```

RESULT 35
; Sequence 15, Application US/09812633
; Patent No. US20020147996A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; APPLICANT: Li, Dawei
; APPLICANT: Mok, Samuel C.
; APPLICANT: Cramer, Daniel W.
; APPLICANT: Ma, Yupo
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/066001
; CURRENT APPLICATION NUMBER: US/09/812,633
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: US 60/216,723
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: derived from Polyoma virus large T antigen
US-09-812-633-15
```

```

Query Match          0.5%; Score 7; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy          326 QEGDDPL 332
Db          3 QEGDDPL 9
```

```

RESULT 36
US-09-988-117-15
; Sequence 15, Application US/09988117
; Patent No. US20020156039A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; APPLICANT: Li, Dawei
; APPLICANT: Mok, Samuel C.
; APPLICANT: Cramer, Daniel W.
; APPLICANT: Ma, Yupo
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/066002
; CURRENT APPLICATION NUMBER: US/09/988,117
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/812,633
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
```

```

; PRIOR APPLICATION NUMBER: US 60/216,723
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: derived from Polyoma virus large T antigen
US-09-988-117-15
```

```

Query Match          0.5%; Score 7; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy          326 QEGDDPL 332
Db          3 QEGDDPL 9
```

```

RESULT 37
US-09-812-471-14
; Sequence 14, Application US/09812471
; Patent No. US20020018765A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; APPLICANT: Li, Dawei
; APPLICANT: Mok, Samuel C.
; APPLICANT: Cramer, Daniel W.
; APPLICANT: Ma, Yupo
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/066002
; CURRENT APPLICATION NUMBER: US/09/812,471
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: US 60/216,723
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: derived from Polyoma virus large T antigen
US-09-812-471-14
```

```

Query Match          0.5%; Score 7; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy          326 QEGDDPL 332
Db          3 QEGDDPL 9
```

```

RESULT 38
US-09-812-633-14
; Sequence 14, Application US/09812633
; Patent No. US20020147996A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; APPLICANT: Li, Dawei
; APPLICANT: Mok, Samuel C.
; APPLICANT: Cramer, Daniel W.
; APPLICANT: Ma, Yupo
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/066001
; CURRENT APPLICATION NUMBER: US/09/812,633
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: US 60/216,723
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
```


LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: derived from Polyoma virus large T antigen
US-09-812-633-14

Query Match 0.5%; Score 7; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPL 332
DB 3 QEGDDPL 9

RESULT 39
US-09-988-117-14
Sequence 14, Application US/09988117
Patent No. US20020156039A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Thomas L.
APPLICANT: Li, Dawei
APPLICANT: Mok, Samuel C.
APPLICANT: Cramer, Daniel W.
APPLICANT: Ma, Yupo
TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
FILE REFERENCE: 00742/066002
CURRENT APPLICATION NUMBER: US/09/988,117
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/812,633
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: US 60/216,723
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: derived from Polyoma virus large T antigen
US-09-988-117-14

Query Match 0.5%; Score 7; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPL 332
DB 3 QEGDDPL 9

RESULT 40
US-09-812-471-13
Sequence 13, Application US/09812471
Patent No. US20020018765A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Thomas L.
TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
FILE REFERENCE: 00742/062002
CURRENT APPLICATION NUMBER: US/09/812,471
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: US 60/216,723
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 16
TYPE: PRT
ORGANISM: Polyoma virus

US-09-812-471-13

Query Match 0.5%; Score 7; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPL 332
DB 3 QEGDDPL 9

RESULT 41
US-09-812-633-13
Sequence 13, Application US/09812633
Patent No. US20020147996A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Thomas L.
APPLICANT: Li, Dawei
APPLICANT: Mok, Samuel C.
APPLICANT: Cramer, Daniel W.
APPLICANT: Ma, Yupo
TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
FILE REFERENCE: 00742/066001
CURRENT APPLICATION NUMBER: US/09/812,633
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: US 60/216,723
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 16
TYPE: PRT
ORGANISM: Polyoma virus
US-09-812-633-13

Query Match 0.5%; Score 7; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPL 332
DB 3 QEGDDPL 9

RESULT 42
US-09-988-117-13
Sequence 13, Application US/09988117
Patent No. US20020156039A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Thomas L.
APPLICANT: Li, Dawei
APPLICANT: Mok, Samuel C.
APPLICANT: Cramer, Daniel W.
APPLICANT: Ma, Yupo
TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
FILE REFERENCE: 00742/066002
CURRENT APPLICATION NUMBER: US/09/988,117
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/812,633
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: US 60/216,723
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 16
TYPE: PRT
ORGANISM: Polyoma virus
US-09-988-117-13

Query Match 0.5%; Score 7; DB 10; Length 16;

Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPL 332
DB 3 QEGDDPL 9

RESULT 43
US-09-812-471-10
; Sequence 10, Application US/09812471
; Patent No. US20020018765A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/062002
; CURRENT APPLICATION NUMBER: US/09/812,471
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-812-471-10

Query Match

Best Local Similarity 0.5%; Score 7; DB 9; Length 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPL 332
DB 7 QEGDDPL 13

RESULT 44
US-09-812-633-10
; Sequence 10, Application US/09812633
; Patent No. US2002014796A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; APPLICANT: Mok, Samuel C.
; APPLICANT: Cramer, Daniel W.
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/066001
; CURRENT APPLICATION NUMBER: US/09/812,633
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-812-633-10

Query Match
Best Local Similarity 0.5%; Score 7; DB 10; Length 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPL 332
DB 7 QEGDDPL 13

RESULT 45

US-09-988-117-10
; Sequence 10, Application US/09988117
; Patent No. US20020156039A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; APPLICANT: Mok, Samuel C.
; APPLICANT: Cramer, Daniel W.
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/066002
; CURRENT APPLICATION NUMBER: US/09/988,117
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/812,633
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-988-117-10

Query Match

Best Local Similarity 0.5%; Score 7; DB 10; Length 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPL 332
DB 7 QEGDDPL 13

RESULT 46
US-09-726-643-145
; Sequence 145, Application US/09726643
; Patent No. US2002028449A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 26 Human secreted proteins
; FILE REFERENCE: P2040P1
; CURRENT APPLICATION NUMBER: US/09/726,643
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/15187
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-643-145

Query Match
Best Local Similarity 0.5%; Score 7; DB 9; Length 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1340 ATTAKSL 1346
DB 13 ATTAKSL 19

RESULT 47
US-10-042-141-145
; Sequence 145, Application US/10042141
; Publication No. US2002018503A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 26 Human secreted proteins

FILE REFERENCE: P2040P1
CURRENT APPLICATION NUMBER: US/10/042,141
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/726,643
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/15187
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/137,725
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 199
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 145
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-141-145

Query Match 0.5%; Score 7; DB 14; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1340 ATTAKSL 1346
DB 13 ATTAKSL 19

RESULT 48

US-10-232-286-9
Sequence 9, Application US/10232286
Publication No. US20030143579A1
GENERAL INFORMATION:

APPLICANT: Rothe, Mike
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,286
FILING DATE: 30-Aug-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DUB

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-232-286-9

Query Match 0.5%; Score 7; DB 12; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 216 EHAKFP 222
DB 39 EHAKFP 45

RESULT 49

US-09-071-838-94
Sequence 94, Application US/09071838
Patent No. US20020152501A1
GENERAL INFORMATION:

APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyose, Tomohiro
APPLICANT: Yadegari, Ramon
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Fruit Development in Plants
NUMBER OF SEQUENCES: 324
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,838
FILING DATE: 01-MAY-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Baerian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-086100US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-09-071-838-94

Query Match 0.5%; Score 7; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 621 RLKRFV 627
DB 20 RLKRFV 26

RESULT 50

US-10-138-618-21
Sequence 21, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:

APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP

STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996

Query Match 0.54; Score 7; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 EHAKMP 222
Db 29 EHAKMP 35

RESULT 51
US-10-138-618-22
Sequence 22, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, David C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996

US-10-138-618-21
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
MOLECULE TYPE: protein
TOPOLOGY: linear
STRANDEDNESS: <Unknown>
LENGTH: 50 amino acids
TYPE: amino acid
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7176
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-138-618-22

Query Match 0.54; Score 7; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 EHAKMP 222
Db 29 EHAKMP 35

RESULT 52
US-10-138-618-31
Sequence 31, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, David C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7176
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-138-618-31

Query Match 0.54; Score 7; DB 15; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 EHAKWPP 222
Db 29 EHAKWPP 35

RESULT 53
US-10-213-512-94

Sequence 94, Application US/10213512
Publication No. US20030110536A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramon
APPLICANT: Margosheian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
FILE REFERENCE: 023070-086110US
CURRENT APPLICATION NUMBER: US/10/213,512
CURRENT FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: US/09/177,206
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: US 09/071,838
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 94
LENGTH: 50
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-10-213-512-94

Query Match 0.5%; Score 7; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 621 RLKPMV 627
Db 20 RLKPMV 26

RESULT 54
US-09-864-761-43582

Sequence 43582, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 43582

LENGTH: 52

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC004123.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.78

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.53

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.75

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.77

US-09-864-761-43582

Query Match 0.5%; Score 7; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 EEEQKE 45
Db 11 EEEQKE 17

RESULT 55

US-09-864-761-47236
Sequence 47236, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27

```

PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 47236
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC003049.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.87
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.66
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.63
US-09-864-761-47236

```

```

Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 39 EEEEOKE 45
DB 15 EEEEOKE 21

```

```

RESULT 56
US-10-156-761-8279
Sequence 8279, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8279
LENGTH: 56

```

```

TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-8279

```

```

Query Match
Best Local Similarity 100.0%; Score 7; DB 15; Length 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 102 LILFGAG 108
DB 12 LILFGAG 18

```

```

RESULT 57
US-10-156-761-8496
Sequence 8496, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8496
LENGTH: 56
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-8496

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Query Match
Best Local Similarity 100.0%; Score 7; DB 15; Length 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 102 LILFGAG 108
DB 12 LILFGAG 18

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RESULT 58
US-09-864-761-46549
Sequence 46549, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENEOME-DRIVEN SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmics-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27

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; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46549
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AI078461.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: SWISSPROT HIT: Q61687, EVALUATE 3.40e-02
; OTHER INFORMATION: EST_HUMAN HIT: AF114027.1, EVALUATE 1.00e-30
; US-09-864-761-46549
Query Match 0.5%; Score 7; DB 9; Length 64;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 822 ENISEND 828
DB 17 ENISEND 23
RESULT 59
US-09-864-761-43318
; Sequence 43318, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmeca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43318
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004123.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
; OTHER INFORMATION: EST_HUMAN HIT: R60198.1, EVALUATE 5.70e+00
; OTHER INFORMATION: SWISSPROT HIT: P03518, EVALUATE 5.90e+00
; US-09-864-761-43318
Query Match 0.5%; Score 7; DB 9; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1205 FISLKIL 1211
DB 22 FISLKIL 28
RESULT 60
US-09-201-936-23
; Sequence 23, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Bald, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; PRIOR FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
```

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; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 23
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-23

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Query Match
Best Local Similarity 0.5%; Score 7; DB 10; Length 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 339 FPNCPL 345
Db 61 FPNCPL 67

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RESULT 61
US-09-201-936-27
; Sequence 27, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 27
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-27

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Query Match
Best Local Similarity 0.5%; Score 7; DB 10; Length 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 216 EHAAMP 222
Db 57 EHAAMP 63

```

```

RESULT 62
US-10-041-859-15
; Sequence 15, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND

```

```

; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 15
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Spodoptera frugiperda
US-10-041-859-15

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Query Match
Best Local Similarity 0.5%; Score 7; DB 15; Length 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 284 SFKMPR 290
Db 7 SFKMPR 13

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RESULT 63
US-10-041-859-16
; Sequence 16, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: MAEDA, SUSUMU
; APPLICANT: DEVERAUX, QUINN L.
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 16
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Trichoplusia ni
US-10-041-859-16

```

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Query Match
Best Local Similarity 0.5%; Score 7; DB 15; Length 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 284 SFKMPR 290
Db 7 SFKMPR 13

```

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RESULT 64
US-09-864-761-44802
; Sequence 44802, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenpeng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456

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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44802
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC025516.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.87
; OTHER INFORMATION: SWISSPROT HIT: Q9WU03, EVALU8 4.00e-07
; OTHER INFORMATION: EST_HUMAN HIT: ANS01874.1, EVALU8 4.20e+00
; US-09-864-761-44802
Query Match
Best Local Similarity 0.5%; Score 7; DB 9; Length 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1374 LNMVNER 1380
DB 5 LNMVNER 11
RESULT 65
US-10-106-698-4757
; Sequence 4757, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137

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; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 4757
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-106-698-4757
Query Match
Best Local Similarity 0.5%; Score 7; DB 15; Length 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1073 LITLPSL 1079
DB 20 LITLPSL 26
RESULT 66
US-10-029-386-30446
; Sequence 30446, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; FILE REFERENCE: ABOICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30446
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR22.124.0
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.61
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.93
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.66
; OTHER INFORMATION: SWISSPROT HIT: P36151, EVALU8 6.00e-03
; US-10-029-386-30446
Query Match
Best Local Similarity 0.5%; Score 7; DB 12; Length 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 ELSSALG 28
DB 60 ELSSALG 66
RESULT 67
US-09-864-761-38254
; Sequence 38254, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeoica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04

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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 38254
LENGTH: 99
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC010680.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EST HUMAN HIT: F35989.1, EVALUATE 1.00e-23
US-09-864-761-34814
Query Match
Best Local Similarity 0.5%; Score 7; DB 9; Length 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 857 SWVSEHL 863
DB 50 SWVSEHL 56
RESULT 68
US-09-864-761-34814
Sequence 34814, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenhang
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 34814
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006946.18
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.9
OTHER INFORMATION: EST HUMAN HIT: BE280799.1, EVALUATE 1.00e-32
US-09-864-761-34814
Query Match
Best Local Similarity 0.5%; Score 7; DB 9; Length 101;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 ELNALIG 28
DB 60 ELNALIG 66
RESULT 69
US-09-864-761-39550
Sequence 39550, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
```

APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aesomica-X-1
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US/09/864,761
 PRIOR FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 39550
 LENGTH: 102
 TYPE: PRT
 ORGANISM: Homo sapiens
 PEPTIDE:
 OTHER INFORMATION: MAP TO AC004752.1
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
 OTHER INFORMATION: EXPRESSED IN PETAL, LIVER, SIGNAL = 2.1
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
 OTHER INFORMATION: SWISSPROT HIT: P18168, EVALUATE 4.60e+00
 US-09-864-761-39550

Query Match 0.5%; Score 7; DB 9; Length 102;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 RLRKFMV 627
 |||||
 DB 4 RLRKFMV 10

RESULT 70
 US-10-156-761-8010
 ; Sequence 8010, Application US/10156761

Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIYUKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 8010
 LENGTH: 107
 TYPE: PRT
 ORGANISM: Streptomyces avermitilis
 US-10-156-761-8010

Query Match 0.5%; Score 7; DB 15; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 AVGVVAL 299
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 DB 32 AVGVVAL 38

RESULT 71
 US-09-867-550-1404
 ; Sequence 1404, Application US/09867550
 ; Patent No. US20020082206A1
 GENERAL INFORMATION:
 APPLICANT: Leach, Martin D.
 APPLICANT: Mehraban, Foad,
 APPLICANT: Conley, Pamela
 APPLICANT: Law, Debbie
 APPLICANT: Topper, James
 TITLE OF INVENTION: No. US20020082206A1e1 Polynucleotides from Atherogenic Cells and
 FILE REFERENCE: 21402-013 (Cura-313)
 CURRENT APPLICATION NUMBER: US/09/867,550
 CURRENT FILING DATE: 2001-09-20
 PRIOR APPLICATION NUMBER: USSN 60/208,427
 PRIOR FILING DATE: 2000-05-30
 PRIOR APPLICATION NUMBER: 2125
 NUMBER OF SEQ ID NOS: 2125
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1404
 LENGTH: 109
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-867-550-1404

Query Match 0.5%; Score 7; DB 9; Length 109;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1237 LEEHLIP 1243
 |||||
 DB 36 LEEHLIP 42

RESULT 72
 US-10-029-386-32489
 ; Sequence 32489, Application US/10029386
 ; Publication No. US20030194704A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharon G.

```

APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
FILE REFERENCE: AEWICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Detecting Engine vers. 1.1
SEQ ID NO 32489
LENGTH: 130
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL132642.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: SWISSPROT HIT: P48187, EVALU 1.30e+00
US-10-029-386-32489

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Query Match
Best Local Similarity 0.5%; Score 7; DB 12; Length 130;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1263 HCURVUS 1269
89 HCURVUS 95

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RESULT 73

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US-10-287-274-415
Sequence 415, Application US/10287274
Publication No. US20030181408A1
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allym
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETC
FILE REFERENCE: ELITRA.008DV1
CURRENT APPLICATION NUMBER: US/10/287,274
PRIOR FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: US 09/711164
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 415
LENGTH: 134
TYPE: PRT
ORGANISM: Escherichia coli
US-10-287-274-415

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Query Match
Best Local Similarity 0.5%; Score 7; DB 12; Length 134;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 19 LPELSA 25
86 LPELSA 92

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RESULT 74

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US-09-815-242-5364
Sequence 5364, Application US/09815242
Patent No. US2002061559A1
GENERAL INFORMATION:
APPLICANT: Habelbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.

```

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APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5364
LENGTH: 139
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5364

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Query Match

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Best Local Similarity 0.5%; Score 7; DB 9; Length 139;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1060 ISKLELS 1066
85 ISKLELS 91

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RESULT 75

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US-10-156-761-14388
Sequence 14388, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14388
LENGTH: 144
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-14388

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Query Match

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Best Local Similarity 0.5%; Score 7; DB 15; Length 144;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 31 AVOLAKE 37
109 AVOLAKE 115

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Thu Dec 18 09:31:08 2003

us-09-830-338-1.01igo.rapp

Page 29

Search completed: December 18, 2003, 09:26:17
UOB time : 288 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 09:11:49 / Search time 60 Seconds
(without alignments)
3711.556 Million cell updates/sec

Title: US-09-830-338-1

Perfect score: 1403

Sequence: 1 MATQKASDERISQFDHNL.....SKYLTLIQKWLPSPIQK 1403

Scoring table: OIIGO

Gapop 60.0, Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1403	100.0	1403	AAW20032	Neuronal apoptosis
2	1403	100.0	1403	AAW14079	Genodactrophic Hormo
3	1403	100.0	1403	AAW09539	Human apoptosis in
4	1403	100.0	1403	AAW88053	Human Nalp protein
5	1403	100.0	1403	ABP2166	Human Nalp protein
6	1403	100.0	1403	ABU07400	Protein inhibitor of
7	1282	91.4	1295	AAW14080	Genodactrophic Hormo
8	1282	91.4	1295	AAW09540	Human apoptosis in
9	1084	77.3	1403	AAW20033	Neuronal apoptosis

10	946	67.4	1232	11	AAW98217	Neuronal apoptosis
11	75	5.3	118	21	AAW53493	Human colon cancer
12	60	4.3	60	21	AAW01849	Human secreted pro
13	25	1.8	31	22	AAW12411	Human polypeptide
14	22	1.6	37	22	ABG55972	Human liver peptid
15	22	1.6	37	22	AAW74180	Human bone marrow
16	22	1.6	37	22	AAW34307	Peptide #8344 enco
17	22	1.6	37	23	ABG44119	Human polypeptide
18	9	0.6	67	22	AAW06778	Human polypeptide
19	9	0.6	210	24	ABP81447	Streptococcus pneu
20	9	0.6	210	24	ABU02180	S. pneumoniae type
21	9	0.6	341	21	AAW28074	Arabidopsis thalia
22	9	0.6	349	22	AAW65694	Novel protein kina
23	9	0.6	350	22	AAW03542	Human protein kina
24	9	0.6	350	23	ABP69792	Human polypeptide
25	9	0.6	459	21	AAW28073	Human polypeptide
26	9	0.6	469	21	AAW28072	Arabidopsis thalia
27	8	0.6	15	23	AAW17965	Polyma virus larg
28	8	0.6	56	22	AAW83576	Human immune/hema
29	8	0.6	64	22	ABW50632	Human secreted pro
30	8	0.6	95	21	AAW54291	Human pancreatic c
31	8	0.6	113	22	AAU42144	Propionibacterium
32	8	0.6	152	21	AAW07152	Arabidopsis thalia
33	8	0.6	197	22	ABW61125	Arabidopsis thalia
34	8	0.6	232	21	AAW07151	Arabidopsis thalia
35	8	0.6	232	21	AAW53554	Arabidopsis thalia
36	8	0.6	239	21	AAW07150	Arabidopsis thalia
37	8	0.6	239	21	AAW53553	Human colon cancer
38	8	0.6	259	21	AAW53281	Human polypeptide
39	8	0.6	358	21	AAW07235	Arabidopsis thalia
40	8	0.6	358	21	AAW48600	Arabidopsis thalia
41	8	0.6	358	21	AAW19745	Mouse inhibitor of
42	8	0.6	358	21	AAW19745	Mouse inhibitor of
43	8	0.6	373	21	AAW48599	Mouse inhibitor of
44	8	0.6	374	21	AAW07234	Arabidopsis thalia
45	8	0.6	428	12	AAW12352	Toxoplasma gondii
46	8	0.6	441	20	AAW34752	Chlamydia pneumonia
47	8	0.6	496	18	AAW19745	Mouse inhibitor of
48	8	0.6	496	18	AAW19745	Mouse inhibitor of
49	8	0.6	496	19	AAW63297	Murine XIAP protei
50	8	0.6	496	23	AAW65665	Mouse inhibitor of
51	8	0.6	496	24	ABP72157	Mouse inhibitor of
52	8	0.6	506	23	ABP41530	Human ovarian anti
53	8	0.6	519	22	ABG09940	Novel human diagno
54	8	0.6	521	22	ABW61920	Drosophila melanog
55	8	0.6	523	15	AAW71976	Pertussis A. Bord
56	8	0.6	538	22	ABW67078	Drosophila melanog
57	8	0.6	567	20	AAW88788	Polypeptide fragme
58	8	0.6	567	22	AAW50625	Human secreted pro
59	8	0.6	568	21	AAW85658	Human Actinus S pro
60	8	0.6	575	22	ABW71239	Drosophila melanog
61	8	0.6	583	21	AAW85659	Human Actinus S' pr
62	8	0.6	614	22	ABG09939	Novel human diagno
63	8	0.6	654	21	AAW57754	CXS-P66-CXS fusion
64	8	0.6	679	22	ABW71989	Drosophila melanog
65	8	0.6	845	22	AAW73222	Amino acid sequenc
66	8	0.6	848	23	ABG66688	Human novel polype
67	8	0.6	906	23	ABG66687	Human novel polype
68	8	0.6	934	23	ABW91916	Herbicideally activ
69	8	0.6	968	18	AAW21721	SH2-A. Homo sapie
70	8	0.6	976	18	AAW26624	Signalling inosito
71	8	0.6	976	18	AAW18327	BRB2 associating p
72	8	0.6	1187	18	AAW14002	Mouse SH2-containi
73	8	0.6	1187	18	AAW14003	Human SH2-containi
74	8	0.6	1189	18	AAW26623	Signalling inosito
75	8	0.6	1341	21	AAW85657	Human Actinus L pro
76	8	0.6	1342	22	ABG09943	Novel human diagno
77	8	0.6	2097	22	ABG09944	Novel human diagno
78	8	0.5	7	22	AAW45906	H11 binding site c
79	8	0.5	7	22	AAW45911	H11 binding site c
80	8	0.5	7	22	AAW45916	H11 binding site c
81	7	0.5	10	23	AAW17960	Polyma virus larg
82	7	0.5	14	23	AAW17959	Polyma virus larg

QY 1021 MTVESASORIEHLNHSRPFIESIRPALELSKASVTKCSISKLELSAEBELTLTLPSE 1080
 DB 1021 MTVESASORIEHLNHSRPFIESIRPALELSKASVTKCSISKLELSAEBELTLTLPSE 1080
 QY 1081 SLEVSSTIOSODQIPFNLDFKELCKELSVLESGNINVSVPISPEEPFNHHEKLLIOISA 1140
 DB 1081 SLEVSSTIOSODQIPFNLDFKELCKELSVLESGNINVSVPISPEEPFNHHEKLLIOISA 1140
 QY 1141 EYDSKIVKLIQNSPNLHVFLKCNFSPDGSMTMLVSCCKLATEIKRSDSPFOAVPVA 1200
 DB 1141 EYDSKIVKLIQNSPNLHVFLKCNFSPDGSMTMLVSCCKLATEIKRSDSPFOAVPVA 1200
 QY 1201 SLPNFIKILINLEGQOPDEETSEKFAVILGSLSVLEELIPTGDIYVAKLIIQQCQ 1260
 DB 1201 SLPNFIKILINLEGQOPDEETSEKFAVILGSLSVLEELIPTGDIYVAKLIIQQCQ 1260
 QY 1261 QLHCLRVLSPEKTLNDSVVEIKVAISGSPKLENTLKLSINHKITEGYNPFQALDNM 1320
 DB 1261 QLHCLRVLSPEKTLNDSVVEIKVAISGSPKLENTLKLSINHKITEGYNPFQALDNM 1320
 QY 1321 PNLQELDISRHFTECIKAQATVKSLSQCVLRLPRLIRLNLMLSWLLDADIALNVKER 1380
 DB 1321 PNLQELDISRHFTECIKAQATVKSLSQCVLRLPRLIRLNLMLSWLLDADIALNVKER 1380
 QY 1381 HPOSKYLTIIQKTLIPSPITIQ 1403
 DB 1381 HPOSKYLTIIQKTLIPSPITIQ 1403
 RESULT 2
 ID AAY14079 standard; Protein; 1403 AA.
 AC AAY14079;
 DT 20-JUL-1999 (first entry)
 DE Gonadotropic hormone protein sequence.
 XX Gonadotropic hormone; excessive ovulation animal; transgenic animal;
 KW totipotent cell; somatic cell chromosome.
 OS Homo sapiens.
 PN JP1113444-A.
 PD 27-APR-1999.
 PF 14-OCT-1997; 97JP-0280830.
 PR 14-OCT-1997; 97JP-0280830.
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA (SAKA/) SAKAI H.
 DR MPI: 1999-320709/27.
 DR N-PSDB; AAX58000.
 PT An excessive ovulation animal - useful for improving the
 PT productivity of animals
 XX Claim 3; Page 11-14; 18pp; Japanese.
 CC This sequence represents a gonadotropic hormone.
 CC The invention relates to an excessive ovulation animal, which is a
 CC transgenic animal with a totipotent cell containing a DNA fragment
 CC containing a promoter sequence and a gonadotropic hormone coding
 CC sequence. The DNA fragment is in the somatic cell chromosome. The
 CC excessive ovulation animal is useful for improving the productivity of
 CC animals. The method can improve the productivity of a useful animal.
 SQ Sequence 1403 AA;

Query Match 100.0%; Score 1403; DB 20; Length 1403;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATOQKASDERISQFPHNLLPELSALLGLDAVOLAKLEEBEERAKAMQKYNOSMRSE 60
 DB 1 MATOQKASDERISQFPHNLLPELSALLGLDAVOLAKLEEBEERAKAMQKYNOSMRSE 60
 QY 61 AKRKTFTVTEBPSSNIPDEMAAGPFGVSGIQCCSLIIFGGLTRLPEDHKRF 120
 DB 61 AKRKTFTVTEBPSSNIPDEMAAGPFGVSGIQCCSLIIFGGLTRLPEDHKRF 120
 QY 121 HPDGFLLANDVGNIAKYDIRVKNLKSRLRGCKMYOEERARLASPRNPPYVQGISPCV 180
 DB 121 HPDGFLLANDVGNIAKYDIRVKNLKSRLRGCKMYOEERARLASPRNPPYVQGISPCV 180
 QY 181 LSEBGFPTCKQPTVCCFCGCGCIGNWEBCDPMKHAAMPKCEPLRSKSSSEITROYI 240
 DB 181 LSEBGFPTCKQPTVCCFCGCGCIGNWEBCDPMKHAAMPKCEPLRSKSSSEITROYI 240
 QY 241 QSYKGFVDITGEHFVNSWYQRELPMAASAYCNDISPAVEBELRDSFKOMPRESAVGAVALA 300
 DB 241 QSYKGFVDITGEHFVNSWYQRELPMAASAYCNDISPAVEBELRDSFKOMPRESAVGAVALA 300
 QY 301 KAGLFTYGTIDIVQCSGCGCLEKQOEGDPLDHTRCFRNCPFLQNMKSSAEVTPLOS 360
 DB 301 KAGLFTYGTIDIVQCSGCGCLEKQOEGDPLDHTRCFRNCPFLQNMKSSAEVTPLOS 360
 QY 361 RGEICELLETTSSESNLEDSIAVGPVPEMAQOEAQFQEAQNLNEOLRAAVTSAPFHMMS 420
 DB 361 RGEICELLETTSSESNLEDSIAVGPVPEMAQOEAQFQEAQNLNEOLRAAVTSAPFHMMS 420
 QY 421 LLDISSDLATDHLGGDLSIASRHTSKPQOEPVLNPEFYGLNSVMVCBEGAGSKTVLL 480
 DB 421 LLDISSDLATDHLGGDLSIASRHTSKPQOEPVLNPEFYGLNSVMVCBEGAGSKTVLL 480
 QY 481 KKIAPLWASGCCPLNRPOLVFLVLSSTRPDEGLASIIICDOLLEKGSVTEMCMRNIIQ 540
 DB 481 KKIAPLWASGCCPLNRPOLVFLVLSSTRPDEGLASIIICDOLLEKGSVTEMCMRNIIQ 540
 QY 541 QLNQOVLFLDDYKEICSIPOVIGKLIQNMHSKICLHARADIRRYLFTLIEIK 600
 DB 541 QLNQOVLFLDDYKEICSIPOVIGKLIQNMHSKICLHARADIRRYLFTLIEIK 600
 QY 601 AAPPYNTVCILRLFSHNMTRLRKEMVYFGKXOSLOKIOKTPLEVAALICAMFQYPPDS 660
 DB 601 AAPPYNTVCILRLFSHNMTRLRKEMVYFGKXOSLOKIOKTPLEVAALICAMFQYPPDS 660
 QY 661 FDDVAVFKSYMERLSIRNKATJAEILKATVSSCGEALAGFSCCEPFRDDDLAEGVDED 720
 DB 661 FDDVAVFKSYMERLSIRNKATJAEILKATVSSCGEALAGFSCCEPFRDDDLAEGVDED 720
 QY 721 EDLTMCMASKFTQRLRPYRPLSPAFQEBLAGMELIELDSDROEHODLGLYHLKQINS 780
 DB 721 EDLTMCMASKFTQRLRPYRPLSPAFQEBLAGMELIELDSDROEHODLGLYHLKQINS 780
 QY 781 PMMTVSAVNNFLAVYSSLPSTKAGPKIVSHLHLDVNDKESLENTSEBDVYLKQPRISIQ 840
 DB 781 PMMTVSAVNNFLAVYSSLPSTKAGPKIVSHLHLDVNDKESLENTSEBDVYLKQPRISIQ 840
 QY 841 MQLIRGLMOICPOAYSVMSVSEHLVYALKTAQSVNTVAACSPVILQFLOGRTLLTGALNT 900
 DB 841 MQLIRGLMOICPOAYSVMSVSEHLVYALKTAQSVNTVAACSPVILQFLOGRTLLTGALNT 900
 QY 901 OYFDPHESLSILSRHFPRLRGKTSPRHSEVLETCRDKSOPFLIIOODVSAFEPNNEM 960
 DB 901 OYFDPHESLSILSRHFPRLRGKTSPRHSEVLETCRDKSOPFLIIOODVSAFEPNNEM 960
 QY 961 ERNLAEKEDNVKSYNDMORRASPDLSTGYMKLSPKQYKICPLEVDVNDIDVQDMLIEL 1020
 DB 961 ERNLAEKEDNVKSYNDMORRASPDLSTGYMKLSPKQYKICPLEVDVNDIDVQDMLIEL 1020
 QY 1021 MTVESASORIEHLNHSRPFIESIRPALELSKASVTKCSISKLELSAEBELTLTLPSE 1080

DB 1021 MTFVSAQRIBELHNSGRFIESIRPALBELSKASVTKSISKLELSAABOELLTPSL 1080
 QY 1081 SLEVSQTTOSQDOIFPNLDKFLCLKELSVDELKGNINVSVPDEFEPFHMEKLLIQISA 1140
 DB 1081 SLEVSQTTOSQDOIFPNLDKFLCLKELSVDELKGNINVSVPDEFEPFHMEKLLIQISA 1140
 QY 1141 EYDSKLVKVLKIONSPPNHLKCNFSDPSGLMTMLVSCKULTEIKFSDSFFQAVPVA 1200
 DB 1141 EYDSKLVKVLKIONSPPNHLKCNFSDPSGLMTMLVSCKULTEIKFSDSFFQAVPVA 1200
 QY 1201 SLPMPLIKLILNEGQFPDEETSEKFAVYIIGLSNLEELILPTGDIIRVAKLLIQCC 1260
 DB 1201 SLPMPLIKLILNEGQFPDEETSEKFAVYIIGLSNLEELILPTGDIIRVAKLLIQCC 1260
 QY 1261 QHCLRLVLSFFKTLANDSVVEIAKVAISGFGKLENLKLSINHKITTEGYNFQALDM 1320
 DB 1261 QHCLRLVLSFFKTLANDSVVEIAKVAISGFGKLENLKLSINHKITTEGYNFQALDM 1320
 QY 1321 PNLQELDISRHFTCKKQATTVKSLGCTVLRLPRLIRLMLSLDADIALINVKER 1380
 DB 1321 PNLQELDISRHFTCKKQATTVKSLGCTVLRLPRLIRLMLSLDADIALINVKER 1380
 QY 1381 HPQSKLTLLQKWLIPSPITIQK 1403
 DB 1381 HPQSKLTLLQKWLIPSPITIQK 1403

RESULT 3

AA109539 standard; Protein; 1403 AA.

AA109539;

DT 20-JUL-1999 (first entry)

XX Human apoptosis inhibiting protein #1.

XX Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;

XX epinal muscular atrophy.

XX Homo sapiens.

XX JPI1116599-A.

XX 27-APR-1999.

XX 14-OCT-1997; 97JP-0280831.

XX 14-OCT-1997; 97JP-0280831.

XX (KAGAKU) KAGAKU GIUTSU SHINKO JIGYODAN.

XX WPI; 1999-323531/27.

XX N-PSDB; AAK56272.

XX New apoptosis inhibitory protein - useful for determining mechanism

XX of various apoptotic diseases e.g. human spinal muscular atrophy

XX Claim 1; Page 4-8; 16pp; Japanese.

XX The present sequence represents a human apoptosis inhibitory protein.

XX CC the mechanism of various apoptotic diseases such as human spinal

XX CC muscular atrophy and the diagnosis, the prevention and the treatment

XX of such diseases.

XX Sequence 1403 AA;

Query Match 100.0%; Score 1403; DB 20; Length 1403;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATQKASDERISQDPNHLPELSALLGLDAVOLAKELEBEOKERAKQGYNSQNRSE 60
 DB 1 MATQKASDERISQDPNHLPELSALLGLDAVOLAKELEBEOKERAKQGYNSQNRSE 60
 QY 61 AKKLKFTVYEBYSWIMIQEMAAAGFYFTVGKGIQCCFCSLLTGAGLTPLFEDHKRP 120
 DB 61 AKKLKFTVYEBYSWIMIQEMAAAGFYFTVGKGIQCCFCSLLTGAGLTPLFEDHKRP 120
 QY 121 HPDCGLFLKNDGNIAKYDIRVKNLSRLRGGMRYQSEBARLASFRMPFPYQGISPCV 180
 DB 121 HPDCGLFLKNDGNIAKYDIRVKNLSRLRGGMRYQSEBARLASFRMPFPYQGISPCV 180
 QY 181 LSRAGFVTPGQDVTVOCHSGGCLGNMBEGDDPMKHAAMPKCEPLRSKSSSEETIYI 240
 DB 181 LSRAGFVTPGQDVTVOCHSGGCLGNMBEGDDPMKHAAMPKCEPLRSKSSSEETIYI 240
 QY 241 QSYKGFVDITGEHFVNSWQRELPMAAAYCNDSTPAYEELRLSFRMPFPYQGISPCV 300
 DB 241 QSYKGFVDITGEHFVNSWQRELPMAAAYCNDSTPAYEELRLSFRMPFPYQGISPCV 300
 QY 301 KAGLFYTGIRKDIQVOCFSCGCLERKQEGDDPLDHTQCFNCPFLONMKSABAVTPIQS 360
 DB 301 KAGLFYTGIRKDIQVOCFSCGCLERKQEGDDPLDHTQCFNCPFLONMKSABAVTPIQS 360
 QY 361 RGEICHELLETTESNLEDGIANGPIVPEMAQGEAMPQEAQNLEQLRAAYTSAFRMS 420
 DB 361 RGEICHELLETTESNLEDGIANGPIVPEMAQGEAMPQEAQNLEQLRAAYTSAFRMS 420
 QY 421 LLDISDLATDHLGCDLSIASKHSKVPGLVPEVGNINSVWCVGEGAGSGKTVLL 480
 DB 421 LLDISDLATDHLGCDLSIASKHSKVPGLVPEVGNINSVWCVGEGAGSGKTVLL 480
 QY 481 KKIAPLMAAGCCPLNRFQVLYSLSTRPDGASIIICDOLKEKESVTTEMCMRIIQ 540
 DB 481 KKIAPLMAAGCCPLNRFQVLYSLSTRPDGASIIICDOLKEKESVTTEMCMRIIQ 540
 QY 541 QLNQVLFLLDDYKXICSIPOVIGKLIQKNHLSRTCLLAVATNRARDIRRYLETTIEIK 600
 DB 541 QLNQVLFLLDDYKXICSIPOVIGKLIQKNHLSRTCLLAVATNRARDIRRYLETTIEIK 600
 QY 601 APPFTYVCIILKULPSHNMTRLRKFMVYFGKQISLOKTPPLFAAIQAHMFOYPPDS 660
 DB 601 APPFTYVCIILKULPSHNMTRLRKFMVYFGKQISLOKTPPLFAAIQAHMFOYPPDS 660
 QY 661 FDDVAVFKSYMERLSLRNKATFELIKATVSSGCEALALGFSSCCFENDDDLAEAGVDE 720
 DB 661 FDDVAVFKSYMERLSLRNKATFELIKATVSSGCEALALGFSSCCFENDDDLAEAGVDE 720
 QY 721 EDLTMCKSKFTAGORAPFYRFLSPAFOEFLAGRELIELDSROEHODLGYHLKQINS 780
 DB 721 EDLTMCKSKFTAGORAPFYRFLSPAFOEFLAGRELIELDSROEHODLGYHLKQINS 780
 QY 781 PMHTYSANNFLNVSLSPTAGPKIVSHLHLVDNKESLENISSENDYLLHQEPEISLO 840
 DB 781 PMHTYSANNFLNVSLSPTAGPKIVSHLHLVDNKESLENISSENDYLLHQEPEISLO 840
 QY 841 MQLRGLMOICPOAYSMVSEHLVLAALKTAYOSNTVAACSPVLOFLOGRTLLTGALNT 900
 DB 841 MQLRGLMOICPOAYSMVSEHLVLAALKTAYOSNTVAACSPVLOFLOGRTLLTGALNT 900
 QY 901 QYFDPHESLSLSHPIPIGKNTSPRAHFSVLETCFPGKQVPTIDODVYASFPANNEW 960
 DB 901 QYFDPHESLSLSHPIPIGKNTSPRAHFSVLETCFPGKQVPTIDODVYASFPANNEW 960
 QY 961 BRNLAKEKNVNSYNDMORASPDLSGYWKLSPKQYKIPCLEVDVNDIDVVGDMLEIL 1020
 DB 961 BRNLAKEKNVNSYNDMORASPDLSGYWKLSPKQYKIPCLEVDVNDIDVVGDMLEIL 1020
 QY 1021 MTFVSAQRIBELHNSGRFIESIRPALBELSKASVTKSISKLELSAABOELLTPSL 1080
 DB 1021 MTFVSAQRIBELHNSGRFIESIRPALBELSKASVTKSISKLELSAABOELLTPSL 1080
 QY 1081 SLEVSQTTOSQDOIFPNLDKFLCLKELSVDELKGNINVSVPDEFEPFHMEKLLIQISA 1140

Db 841 MQLAGLMQICPOAVFSSNVEBHLVLALKTAVQSNITVAACSPFVLQFLOGRTLLGALNL 900
 Qy 901 QYFPHPSLISLRSIHPIRGKTSPPRAFSVLETCEKSGVPTIIDDVAAAPENEMK 960
 Db 901 QYFPHPSLISLRSIHPIRGKTSPPRAFSVLETCEKSGVPTIIDDVAAAPENEMK 960
 Qy 961 ERNLAEKEDNVKSYMDQGRASPDLSTGYMKLSPPQYKIPCLAEVNDIVDQDMLETL 1020
 Db 961 ERNLAEKEDNVKSYMDQGRASPDLSTGYMKLSPPQYKIPCLAEVNDIVDQDMLETL 1020
 Qy 1021 MTVSASORIEHLNHSRGPIESIRPALBELSAVYKCSISKELSAEQELMTLPSE 1080
 Db 1021 MTVSASORIEHLNHSRGPIESIRPALBELSAVYKCSISKELSAEQELMTLPSE 1080
 Qy 1081 SLEVSGTIGSODQIFPMLDKFLCLKELSVDEGNINVSVPSEPFPHHMEKLQISA 1140
 Db 1081 SLEVSGTIGSODQIFPMLDKFLCLKELSVDEGNINVSVPSEPFPHHMEKLQISA 1140
 Qy 1141 EYDSKLVKLIQNSPMLHFMHKKNFSDSGSLMTMLVSCKLTETKESGSPQAVPVYA 1200
 Db 1141 EYDSKLVKLIQNSPMLHFMHKKNFSDSGSLMTMLVSCKLTETKESGSPQAVPVYA 1200
 Qy 1201 SLPPFISLKLINLEGOQFPDEESTSEKFAVYIGSLSNLEBELPTGDIYRAVAKLIIOCC 1260
 Db 1201 SLPPFISLKLINLEGOQFPDEESTSEKFAVYIGSLSNLEBELPTGDIYRAVAKLIIOCC 1260
 Qy 1261 QHCLRVLSFEKTLANDSVETAKVAISGFOKLENLKLSINHKTIEBGRPFQALDMM 1320
 Db 1261 QHCLRVLSFEKTLANDSVETAKVAISGFOKLENLKLSINHKTIEBGRPFQALDMM 1320
 Qy 1321 PNIQELDISHEPTECKKQATVKSLSGCCVRLPRLIRLMLSMWLLDADIALMLVMKER 1380
 Db 1321 PNIQELDISHEPTECKKQATVKSLSGCCVRLPRLIRLMLSMWLLDADIALMLVMKER 1380
 Qy 1381 HPOSKYLITLQKMLLPFSPIIOK 1403
 Db 1381 HPOSKYLITLQKMLLPFSPIIOK 1403

RESULT 5
 ABP72166
 ID ABP72166 standard, Protein, 1403 AA.
 AC ABP72166;
 XX 22-APR-2003 (first entry)
 DE Human inhibitor of apoptosis protein NIP.
 KM Inhibitor of apoptosis; NIP; human; apoptosis; cancer; leukemia;
 KM lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic;
 OS Homo sapiens.
 PN MO2003004606-A2.
 PD 16-JAN-2003.
 XX 03-JUL-2002; 2002MO-US21002.
 XX 03-JUL-2001; 2001US-0898158.
 PA (UYCO) UNIV. COLUMBIA NEW YORK.
 PI Troy CM, Shelanski ML;
 DR WPI; 2003-210351/20.
 PT New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
 XX treating cancer, neurodegenerative disorder or cardiomyopathy
 PS Disclosure: Fig 24A-C, 124pp. English.

CC The present sequence is the protein sequence of human inhibitor of
 CC apoptosis protein NIP. The invention provides a nucleic acid,
 CC such as an antisense oligonucleotide, which specifically hybridizes
 CC to a nucleic acid encoding an inhibitor of apoptosis protein,
 CC especially M1AP1, M1AP2, M1AP3, C1AP1, C1AP2 and X1AP. A claimed
 CC method for inducing a cell's death comprises contacting the cell
 CC with the nucleic acid under conditions permitting the nucleic acid
 CC to enter the cell, especially the use of a vector, liposome, or a
 CC mechanical or electrical means. The method is used to treat acute
 CC lymphocytic leukemia, acute myelogenous leukemia, lung cancer,
 CC breast cancer, ovarian cancer, prostate cancer, lymphoma, Hodgkin's
 CC disease, malignant melanoma, neuroblastoma, renal cell carcinoma
 CC and squamous cell carcinoma (all claimed).

Sequence 1403 AA:

Query Match 100.0%; Score 1403; DB 24; Length 1403;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATQKASDRIISQFPHNLPELSALGLDAVQAKLEBEQEKERAKMGYNSQMRSE 60
 Db 1 MATQKASDRIISQFPHNLPELSALGLDAVQAKLEBEQEKERAKMGYNSQMRSE 60
 Qy 61 AKRLKTVTEPYSSWIPOEMAAAGFTGVKSGIOGCCSLIFGAGLTRLPIDHKRF 120
 Db 61 AKRLKTVTEPYSSWIPOEMAAAGFTGVKSGIOGCCSLIFGAGLTRLPIDHKRF 120
 Qy 121 HPOCGFLNNDGNINAKYDIRYKNIKSLRGCKKRYOBEERARLASFRNPPYVGISPCV 180
 Db 121 HPOCGFLNNDGNINAKYDIRYKNIKSLRGCKKRYOBEERARLASFRNPPYVGISPCV 180
 Qy 181 LSEAGVFTGKODTVVOCSCGCLGNMEGGDPWKEHAKNPFCEPLRAKKSSEITQYI 240
 Db 181 LSEAGVFTGKODTVVOCSCGCLGNMEGGDPWKEHAKNPFCEPLRAKKSSEITQYI 240
 Qy 241 QSYKGFVDITGSHFNVNVORELPMASAYCNDISFAVEBELDPSFDWYREBAVVALA 300
 Db 241 QSYKGFVDITGSHFNVNVORELPMASAYCNDISFAVEBELDPSFDWYREBAVVALA 300
 Qy 301 KAGLFTYTGKIDIVOCFSGCGCLEKMGOGDDPLDHTRCPCNCFLONMKSALEVTPDQS 360
 Db 301 KAGLFTYTGKIDIVOCFSGCGCLEKMGOGDDPLDHTRCPCNCFLONMKSALEVTPDQS 360
 Qy 361 RGEUCLELLETSSENLSDSIIVGPIVEMAQGEAQMFOEAKNQLNQLAAVTSFRMS 420
 Db 361 RGEUCLELLETSSENLSDSIIVGPIVEMAQGEAQMFOEAKNQLNQLAAVTSFRMS 420
 Qy 421 LLDISSDLATDHLGCDLSTASKHISKPVQEPVYLRVEGKINSVNCYEGEAGSGTYLL 480
 Db 421 LLDISSDLATDHLGCDLSTASKHISKPVQEPVYLRVEGKINSVNCYEGEAGSGTYLL 480
 Qy 481 KXIAFLMASGCCPLNRFQVLYTSLSTRPDEGLASIIDQLLEKESVTEMCRNIQ 540
 Db 481 KXIAFLMASGCCPLNRFQVLYTSLSTRPDEGLASIIDQLLEKESVTEMCRNIQ 540
 Qy 541 QLNQVLFLLDYKEICSIPOVIGKLIQKNHLSRTCLLIAYTNARPIRYLLETLEIK 600
 Db 541 QLNQVLFLLDYKEICSIPOVIGKLIQKNHLSRTCLLIAYTNARPIRYLLETLEIK 600
 Qy 601 AEPFYNTVCLIRKLFSSNMTRLRKENVYFGKQNSIQKIQTPLPVAACAHMPQYPPDS 660
 Db 601 AEPFYNTVCLIRKLFSSNMTRLRKENVYFGKQNSIQKIQTPLPVAACAHMPQYPPDS 660
 Qy 661 FDDVAVFKSYWERLSLNKATASILKATVSSCGELALGPFSCCFERNDDDLAEAGVDE 720
 Db 661 FDDVAVFKSYWERLSLNKATASILKATVSSCGELALGPFSCCFERNDDDLAEAGVDE 720
 Qy 721 EDLTMCMSKFTAQRLAPFPYRFLSPAFQELAGMLITLLDSQEQHODIGLYHLKQINS 780
 Db 721 EDLTMCMSKFTAQRLAPFPYRFLSPAFQELAGMLITLLDSQEQHODIGLYHLKQINS 780

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QY 781 PMMTVASANNFLNLYVSLSPSTKASPKIVSHLLHIVDNKESLENTSENDYTLKHQPIRSIQ 840
DB 781 PMMTVASANNFLNLYVSLSPSTKASPKIVSHLLHIVDNKESLENTSENDYTLKHQPIRSIQ 840
QY 841 MOLLIRGLMOICPOAYNSVMSVSEHLVLALKTAVQSNVTAAVSPVLAQPIQGRITTLGALNI 900
DB 841 MOLLIRGLMOICPOAYNSVMSVSEHLVLALKTAVQSNVTAAVSPVLAQPIQGRITTLGALNI 900
QY 901 QYFEFDHESLILSRSHHPPIRGNKTSPPRAHSPVLETCTDKSQVPTIIOODVASAPEPNNEK 960
DB 901 QYFEFDHESLILSRSHHPPIRGNKTSPPRAHSPVLETCTDKSQVPTIIOODVASAPEPNNEK 960
QY 961 ERNLAEREDNVKSYMOMORRASPDLSTGYWKLSPKQYKIPCLBYDVNDIVVQGMLEITL 1020
DB 961 ERNLAEREDNVKSYMOMORRASPDLSTGYWKLSPKQYKIPCLBYDVNDIVVQGMLEITL 1020
QY 1021 MTVFSASQRIETLHANSRGRISIRPALELSKASTKCSIKELSAABOEILLTLPSLE 1080
DB 1021 MTVFSASQRIETLHANSRGRISIRPALELSKASTKCSIKELSAABOEILLTLPSLE 1080
QY 1081 SLEVSQTIOSQDQIFPNLDKFLCLKELSVYLEGNINVSFVLPBEPFNHMEKLLIQISA 1140
DB 1081 SLEVSQTIOSQDQIFPNLDKFLCLKELSVYLEGNINVSFVLPBEPFNHMEKLLIQISA 1140
QY 1141 EYPPSKLYVLKIONSRLNHPHLCNPFSDPSGLMTMLVSCCKLREIKFSDSPQAVPVA 1200
DB 1141 EYPPSKLYVLKIONSRLNHPHLCNPFSDPSGLMTMLVSCCKLREIKFSDSPQAVPVA 1200
QY 1201 SLEPNFSLKLINLEGOQFDEETSEKFAVILGSLNMBELILPTGDSGYVAVAKLIIOQCC 1260
DB 1201 SLEPNFSLKLINLEGOQFDEETSEKFAVILGSLNMBELILPTGDSGYVAVAKLIIOQCC 1260
QY 1261 QHCHLRLVSFFKTLNDVSVEITAKVAISGGFQKLENLKLSTNHKITEGTRNFPQALDNN 1320
DB 1261 QHCHLRLVSFFKTLNDVSVEITAKVAISGGFQKLENLKLSTNHKITEGTRNFPQALDNN 1320
QY 1321 PNIQELDISHNEFTECIKQAATTVKSLSQCVLRLPRLIRLNLMSWLLDADIALINVKER 1380
DB 1321 PNIQELDISHNEFTECIKQAATTVKSLSQCVLRLPRLIRLNLMSWLLDADIALINVKER 1380
QY 1381 HPOSKYTLIOKWLIFPSPPIOK 1403
DB 1381 HPOSKYTLIOKWLIFPSPPIOK 1403

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XX WPI: 2003-058520/05.
DB Novel genes which are differentially regulated in prostate cancer.
XX Useful for diagnosing prostate cancer in prostate tissue sample and
XX assessing therapeutic or preventive intervention in prostate cancer
XX patients.
XX Claim 1; Page 202-206; 416pp; English.
XX The invention describes genes (I) which are differentially regulated in
XX prostate cancer. (I) is useful for diagnosing a prostate cancer in a
XX sample comprising prostate tissue, which involves determining the number
XX of target genes which are differentially-regulated in the sample, where
XX the number is indicative of the probability that the sample comprises
XX prostate cancer. (I) is useful for assessing a therapeutic or preventive
XX intervention in a subject having a prostate cancer, which involves
XX determining the expression levels in a sample comprising prostate tissue
XX of target genes which are differentially-regulated in prostate cancer.
XX Preferably, the expression levels of at least 10 genes are determined.
XX (II) is also useful for identifying agents that modulate a biological
XX activity of a polypeptide differentially-regulated in prostate cancer
XX cells, which involves contacting a polypeptide differentially-regulated
XX in prostate cancer cells with a test agent under conditions effective for
XX the test agent to modulate a biological activity of the polypeptide, and
XX determining whether the test agent modulates the biological activity.
XX (II) is useful as molecular markers, as drug targets, and for detecting,
XX diagnosing, staging, grading, assessing, monitoring, prognosticating,
XX preventing or treating, determining predisposition to diseases and
XX conditions especially relating to prostate cancer. (I) and its expression
XX products are used in the diagnostic test to assay for presence of cancer
XX e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
XX blood etc. (I) is useful for assessing cancer e.g., to determine the type
XX of cancer, its stage of development, the nature of genetic defect, etc.
XX The polypeptide encoded by (I) can be used as target for therapy or drug
XX discovery. (I) can also be used for expressing the polypeptide and thus
XX useful in therapeutic applications to treat prostate cancer. (I) is
XX identification of specific genes, and groups of genes, expressed in
XX pathways physiologically relevant to prostate cancer permits the
XX definition of functional and disease pathways and the delineation of
XX targets in these pathways which are useful in diagnostic, therapeutic,
XX and clinical applications. This is the amino acid sequence of a protein
XX differentially regulated in prostate cancer.
SQ Sequence 1403 AA:
Query Match 100.0%; Score 1403; DB 24; Length 1403;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATQOKASDERISQFDHNLPELSALLGLDAVOALAKLEEBEORERAKMOXGYNQMRSE 60
DB 1 MATQOKASDERISQFDHNLPELSALLGLDAVOALAKLEEBEORERAKMOXGYNQMRSE 60
QY 61 AKRLKFTVTEPSSWITPEMAAAGFYTVKYSIGQCCSLILFGGLRLPLBHKRP 120
DB 61 AKRLKFTVTEPSSWITPEMAAAGFYTVKYSIGQCCSLILFGGLRLPLBHKRP 120
QY 121 HPDQGFLLNKDVGNIAKYDIRVKNLKSRLRGKRYOREBARLASFNNPFPYVQGISPCV 180
DB 121 HPDQGFLLNKDVGNIAKYDIRVKNLKSRLRGKRYOREBARLASFNNPFPYVQGISPCV 180
QY 181 LSRAGFYFTGKQDTPVCCSCGGLNWEEGDDPMKEHAKMFKPKCFIRSKSSSEITQYI 240
DB 181 LSRAGFYFTGKQDTPVCCSCGGLNWEEGDDPMKEHAKMFKPKCFIRSKSSSEITQYI 240
QY 241 QSYKGFVDITGEHFNVSNTQRELPMASAYCNDSTFAYEELRLDSFCWMPRESAVGAALAA 300
DB 241 QSYKGFVDITGEHFNVSNTQRELPMASAYCNDSTFAYEELRLDSFCWMPRESAVGAALAA 300
QY 301 KAGLPYTGIDIVQVSCGGLBKMOEGDDPLDHTRCFPNCPFLQNNKSSASVTPDIQS 360
DB 301 KAGLPYTGIDIVQVSCGGLBKMOEGDDPLDHTRCFPNCPFLQNNKSSASVTPDIQS 360

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Db      301 KAGLFYTGKIDIVQCFSCGCGLEKMOGDDPLDDHTRCFPNCFPLQNMKSSAEVTPDLOS 360
Qy      361 RGEICELLETTSSTSNLEDSIAVGPIVPMAGQEAQWFOEAKNINTEQLRAAYTSAFRRMS 420
Db      361 RGEICELLETTSSTSNLEDSIAVGPIVPMAGQEAQWFOEAKNINTEQLRAAYTSAFRRMS 420
Qy      421 LLDISDPLATDHLGGCDLSIAASKISKVPQEPVLPEVFNINANSUNCVEGEGSGKTVLL 480
Db      421 LLDISDPLATDHLGGCDLSIAASKISKVPQEPVLPEVFNINANSUNCVEGEGSGKTVLL 480
Qy      481 KKIAPLWAGCCPLNRRPOLVFLYLSISTPDDGLASII CDOLLEKESVTMCMRNIIQ 540
Db      481 KKIAPLWAGCCPLNRRPOLVFLYLSISTPDDGLASII CDOLLEKESVTMCMRNIIQ 540
Qy      541 QLNKQVLFLLDYKXICSIPOVIGKLIQKNHLSRTCLIAVTRNARDIRRYETILEIK 600
Db      541 QLNKQVLFLLDYKXICSIPOVIGKLIQKNHLSRTCLIAVTRNARDIRRYETILEIK 600
Qy      601 APPFVNTVCILRKLFSHMTLRKFMVYEGKNSLOKOTPLFVAALCAHWFQYPPDS 660
Db      601 APPFVNTVCILRKLFSHMTLRKFMVYEGKNSLOKOTPLFVAALCAHWFQYPPDS 660
Qy      661 PDDVAVFSSYMERLSIRKATAEILKATVSSCGEELALAGPSCCFEENDDDLAAGVDS 720
Db      661 PDDVAVFSSYMERLSIRKATAEILKATVSSCGEELALAGPSCCFEENDDDLAAGVDS 720
Qy      721 EDLTCLMSKFTTAQRLRPYRPLSPAFOEFLAGMRLIELDSDRQEHQDLGLYHLKOINS 780
Db      721 EDLTCLMSKFTTAQRLRPYRPLSPAFOEFLAGMRLIELDSDRQEHQDLGLYHLKOINS 780
Qy      781 PMWTSAVNNFLANVSSLPTKAGPKIVSHLHLVDNKESEINSENDVYLKROPEISIQ 840
Db      781 PMWTSAVNNFLANVSSLPTKAGPKIVSHLHLVDNKESEINSENDVYLKROPEISIQ 840
Qy      841 MOLLRGLMOJCPOAYSYMSEBHLVLAALKTAQVOSNTVAACSPVLQFLQGRLLTGALNL 900
Db      841 MOLLRGLMOJCPOAYSYMSEBHLVLAALKTAQVOSNTVAACSPVLQFLQGRLLTGALNL 900
Qy      901 QYFDPHESLSLRSHIFIRKNKTSPPAHFSVLETCFDSQVPTIIDQYASAFENMWM 960
Db      901 QYFDPHESLSLRSHIFIRKNKTSPPAHFSVLETCFDSQVPTIIDQYASAFENMWM 960
Qy      961 ERNLAEKEDNVKSYMOMQRRASPDLSITYWKLSPKOYKICOLEVNVNDIDVVGDMLEIL 1020
Db      961 ERNLAEKEDNVKSYMOMQRRASPDLSITYWKLSPKOYKICOLEVNVNDIDVVGDMLEIL 1020
Qy      1021 MTVFSASORIELHLNHSRGFTESIRPALBELSKASVTKCSISKLELSAAEOBELLLTLPSE 1080
Db      1021 MTVFSASORIELHLNHSRGFTESIRPALBELSKASVTKCSISKLELSAAEOBELLLTLPSE 1080
Qy      1081 SLEVSSTIGSQOIFPNLDKFLCKELSVLEGNINVFVIEPEEPFNHMEKLLIOTISA 1140
Db      1081 SLEVSSTIGSQOIFPNLDKFLCKELSVLEGNINVFVIEPEEPFNHMEKLLIOTISA 1140
Qy      1141 EYDPSKLVKLQNSPNLHVFLKCNFSDGSLMTMLVSCCKLTELKSDSFFQAVPFA 1200
Db      1141 EYDPSKLVKLQNSPNLHVFLKCNFSDGSLMTMLVSCCKLTELKSDSFFQAVPFA 1200
Qy      1201 SLPNFSLKIINTEGQOPPEETSEKRAVITIGSLNLEELLPTGDSIYVAALIIQQOQ 1260
Db      1201 SLPNFSLKIINTEGQOPPEETSEKRAVITIGSLNLEELLPTGDSIYVAALIIQQOQ 1260
Qy      1261 QHCHLRVSEFKTLNDSVVEIAKVAISGGFOKLENLKLSINHKTIEGRNFQALNDM 1320
Db      1261 QHCHLRVSEFKTLNDSVVEIAKVAISGGFOKLENLKLSINHKTIEGRNFQALNDM 1320
Qy      1321 PNLQELDISRHFTECIKAQATYKLSQCVLRLPILIRNMLSWLLDADDIALLNVMKR 1380
Db      1321 PNLQELDISRHFTECIKAQATYKLSQCVLRLPILIRNMLSWLLDADDIALLNVMKR 1380
Qy      1381 HPOSKLTIILOKNIILPSPPIOK 1403
Db      1381 HPOSKLTIILOKNIILPSPPIOK 1403
Qy      1381 HPOSKLTIILOKNIILPSPPIOK 1403
Db      1381 HPOSKLTIILOKNIILPSPPIOK 1403

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RESULT 7
AAV14080
ID AAV14080 standard; Protein, 1295 AA.
AC AAV14080;
DT 20-JUL-1999 (first entry)
XX Gonadotropic hormone protein sequence.
XX Gonadotropic hormone; excessive ovulation animal; transgenic animal;
XX totipotent cell; somatic cell chromosome.
XX Homo sapiens.
XX JP11113444-A.
XX 27-APR-1999.
XX 14-OCT-1997; 97JP-0280830.
XX 14-OCT-1997; 97JP-0280830.
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX (SAKA/) SAKAI H.
XX N-PSDB; AAX58001.
XX WPI; 1999-320709/27.
XX An excessive ovulation animal - useful for improving the
XX productivity of animals
XX Claim 3; Page 14-18; 18pp; Japanese.
XX This sequence represents a gonadotropic hormone.
XX The invention relates to an excessive ovulation animal, which is a
XX transgenic animal with a totipotent cell containing a DNA fragment
XX containing a promoter sequence and a gonadotropic hormone coding
XX sequence. The DNA fragment is in the somatic cell chromosome. The
XX excessive ovulation animal is useful for improving the productivity of
XX animals. The method can improve the productivity of a useful animal.
XX Sequence 1295 AA;
XX
Query Match 91.4%; Score 1282; DB 20; Length 1295;
Blast Local Similarity 100.0%; Pred. No. 0;
Matches 1282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MATOOKASDERISQFDHNLPELSALLGDAVOLAKIEEBEOKERAKMQGYSQMRSE 60
Db 1 MATOOKASDERISQFDHNLPELSALLGDAVOLAKIEEBEOKERAKMQGYSQMRSE 60
Qy 61 AKRLKTPVTEPSSWIPOBMAAGFYTGVSIGIOFCCSLILFGAGLTRPIEDHKRF 120
Db 61 AKRLKTPVTEPSSWIPOBMAAGFYTGVSIGIOFCCSLILFGAGLTRPIEDHKRF 120
Qy 121 HPDGFPLANDVNIKYDIRVKNLKSRLRGKRYOEERBARLASFRMPPFYOGISPCV 180
Db 121 HPDGFPLANDVNIKYDIRVKNLKSRLRGKRYOEERBARLASFRMPPFYOGISPCV 180
Qy 181 LSEAGFYFTSKODTVOGCPSCGCGCLANNEEGDDPKKEHAKWPCFELRSKSSSEITQYI 240
Db 181 LSEAGFYFTSKODTVOGCPSCGCGCLANNEEGDDPKKEHAKWPCFELRSKSSSEITQYI 240
Qy 241 QSYKGFVDITGHEFNANVQRELPMAAAYCNDISIPAYEELRLDSFKDMPRESAVGVALA 300
Db 241 QSYKGFVDITGHEFNANVQRELPMAAAYCNDISIPAYEELRLDSFKDMPRESAVGVALA 300
Qy 301 KAGLFYTGKIDIVQCFSCGCGLEKMOGDDPLDDHTRCFPNCFPLQNMKSSAEVTPDLOS 360
Db 301 KAGLFYTGKIDIVQCFSCGCGLEKMOGDDPLDDHTRCFPNCFPLQNMKSSAEVTPDLOS 360

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Qy	361	REBELCELLETTESUNJEDSIIVAGVIVEMQGEKOWOEKXNLNEOLRAVYSAFPRMS	420
Dp	361	REBELCELLETTESUNJEDSIIVAGVIVEMQGEKOWOEKXNLNEOLRAVYSAFPRMS	420
Qy	421	LUDISSDLATDHLACCDLSIASKHI SKRPOEPLVLPVFGNLSVMCEGEASKTVLL	480
Dp	421	LUDISSDLATDHLACCDLSIASKHI SKRPOEPLVLPVFGNLSVMCEGEASKTVLL	480
Qy	481	KXIAFLMASGCCPLNRFOLVFYLSTASTPDELSIIICDOLLEKESGVTEACRNIIO	540
Dp	481	KXIAFLMASGCCPLNRFOLVFYLSTASTPDELSIIICDOLLEKESGVTEACRNIIO	540
Qy	541	OLKNOYFLFLDDYKEICSIPOVIGKLIOKNHLSTCTLLIAVRNBARDIRRYLETILBIK	600
Dp	541	OLKNOYFLFLDDYKEICSIPOVIGKLIOKNHLSTCTLLIAVRNBARDIRRYLETILBIK	600
Qy	601	APPEYNTVCLAKFLPSHMWTRLRKPMYFGNOSLOKIOKTPFLVATICAHHFOYRPPPS	660
Dp	601	APPEYNTVCLAKFLPSHMWTRLRKPMYFGNOSLOKIOKTPFLVATICAHHFOYRPPPS	660
Qy	661	PDDVAVFKSYMERLSLRNKATAELIKATVSSCGELAKGPFSCCFEFNDDIAEAGVBD	720
Dp	661	PDDVAVFKSYMERLSLRNKATAELIKATVSSCGELAKGPFSCCFEFNDDIAEAGVBD	720
Qy	721	EDUTYMCWSKFLPAONLRPPYRFLISPAOERPLAGRULI ELIDSRQSHOLGILYHLKQNS	780
Dp	721	EDUTYMCWSKFLPAONLRPPYRFLISPAOERPLAGRULI ELIDSRQSHOLGILYHLKQNS	780
Qy	781	PMATVSAVNNFNAVYSULPSTRKAGPKIVSHLLIHYDKESLENI SENDYLVKHQOEISLO	840
Dp	781	PMATVSAVNNFNAVYSULPSTRKAGPKIVSHLLIHYDKESLENI SENDYLVKHQOEISLO	840
Qy	841	MOLRLGMOITCQOAFSVSVSHLLVYALAKTAYOSNTVAACSPPYLOPLOGRTLTGALNTL	900
Dp	841	MOLRLGMOITCQOAFSVSVSHLLVYALAKTAYOSNTVAACSPPYLOPLOGRTLTGALNTL	900
Qy	901	QYEFHDEBELSLRBSIHFPRIKGNKTSPPAHSVLETCFDSQVPTLIDOOYASAFPMNEM	960
Dp	901	QYEFHDEBELSLRBSIHFPRIKGNKTSPPAHSVLETCFDSQVPTLIDOOYASAFPMNEM	960
Qy	961	ERNLAEKEDNVKSYNDMQRASPDLSITGYKLSPKOYKICPLEVDVNDIDVYGDMLEIL	1020
Dp	961	ERNLAEKEDNVKSYNDMQRASPDLSITGYKLSPKOYKICPLEVDVNDIDVYGDMLEIL	1020
Qy	1021	MATFASQOEIHELHNSRGTESTRPALMELSKASVYTCSSIKTELSAAOCELLTLPSE	1080
Dp	1021	MATFASQOEIHELHNSRGTESTRPALMELSKASVYTCSSIKTELSAAOCELLTLPSE	1080
Qy	1081	SLEVSCTIGOSQOIFPNLDFKLCLEKESVDLEGNINVSYPVIBEPFNPFMHEKTLIOISA	1140
Dp	1081	SLEVSCTIGOSQOIFPNLDFKLCLEKESVDLEGNINVSYPVIBEPFNPFMHEKTLIOISA	1140
Qy	1141	EXYDPSULVYLIONSFNLLVFFHLKCNFSPEDBSLMTMLVSCUKLTETIKFSDSPQAVPPYA	1200
Dp	1141	EXYDPSULVYLIONSFNLLVFFHLKCNFSPEDBSLMTMLVSCUKLTETIKFSDSPQAVPPYA	1200
Qy	1201	SLPNPISLKIILMBEQOPDEBETSEKFAVYIGSLSNLEELILPTGGIIRAVAKLIIOOCO	1260
Dp	1201	SLPNPISLKIILMBEQOPDEBETSEKFAVYIGSLSNLEELILPTGGIIRAVAKLIIOOCO	1260
Qy	1261	QJHCLARVLSFFKTLINDSVLEI 1282	
Dp	1261	QJHCLARVLSFFKTLINDSVLEI 1282	

XX	Human apoptosis inhibiting protein #2.
DE	
XX	Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;
KM	spinal muscular atrophy.
XX	
OS	Homo sapiens.
XX	JP11116599-A.
XX	
PD	27-APR-1999.
XX	
XX	14-OCT-1997; 97JP-0280831.
XX	
PR	14-OCT-1997; 97JP-0280831.
XX	
PA	(KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
DR	WPI; 1999-123511/27.
XX	
DR	N-FSDB; AAK56273.
PT	New apoptosis inhibitory protein - useful for determining mechanism
XX	of various apoptotic diseases e.g. human spinal muscular atrophy
XX	
PS	Claim 1; Page 8-11; 16pp; Japanese.
XX	
CC	The present sequence represents a human apoptosis inhibitory protein
CC	the apoptosis inhibitory protein is useful for the elucidation of
CC	the mechanism of various apoptosis diseases such as human spinal
CC	muscular atrophy and the diagnosis, the prevention and the treatment
CC	of such diseases.
XX	
XX	Sequence 1295 AA;

RESULT 3	
AA09540	
XX	AA09540 standard; Protein; 1295 AA
AC	
XX	AA09540;
DT	20-JUL-1999 (first entry)

Query Match	91.4%	Score 1282;	DB 20;	Length 1295;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1282;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
QY	1	MATQKASDERISQDTHNLPELSNLIGDAVQAKLELEBEQKAAKQKNGSOMSE	60	
Db	1	MATQKASDERISQDTHNLPELSNLIGDAVQAKLELEBEQKAAKQKNGSOMSE	60	
QY	61	ARKLKFVLYEYSMSIQEMAAAGPYFTGVKSGIQCFCSLLIFAGLTRPIEDHKRF	120	
Db	61	ARKLKFVLYEYSMSIQEMAAAGPYFTGVKSGIQCFCSLLIFAGLTRPIEDHKRF	120	
QY	121	HPDQGLANKDVGNIAKTDIRVKULKSRLNGKMRVQEEBARLASRRMPFYVQISPCV	180	
Db	121	HPDQGLANKDVGNIAKTDIRVKULKSRLNGKMRVQEEBARLASRRMPFYVQISPCV	180	
QY	181	LSBAGVFPGKODTVQCFSCGGLGNNEBGDDPWKEHAKMFKPCBEFLARSKKSEBITQYI	240	
Db	181	LSBAGVFPGKODTVQCFSCGGLGNNEBGDDPWKEHAKMFKPCBEFLARSKKSEBITQYI	240	
QY	241	QSKYGVDTTSGHPFNWVQRELPMASAYCNDSTFAYSELRUDSFQWPRESNVGAALAA	300	
Db	241	QSKYGVDTTSGHPFNWVQRELPMASAYCNDSTFAYSELRUDSFQWPRESNVGAALAA	300	
QY	301	KAGLFTYTGKIDIVQCFSCGGLCKEMQESDDPLDHTKCFPNCKCPFLQNMKSSAEVTPDLOS	360	
Db	301	KAGLFTYTGKIDIVQCFSCGGLCKEMQESDDPLDHTKCFPNCKCPFLQNMKSSAEVTPDLOS	360	
QY	361	RGLTCLLETTSESULBESIAVGPVPEBMQGEBAQWQEAKNINBOLRAAYTSASPRHNS	420	
Db	361	RGLTCLLETTSESULBESIAVGPVPEBMQGEBAQWQEAKNINBOLRAAYTSASPRHNS	420	
QY	421	LIDISSEDLATDHLACDDSIASKHSIKRVPQEPVLPEVPQNLNSVWCVGBAGSGKTVLL	480	
Db	421	LIDISSEDLATDHLACDDSIASKHSIKRVPQEPVLPEVPQNLNSVWCVGBAGSGKTVLL	480	
QY	481	KKIAFLPMAGCCPLNRPQVLYPLYSLSTPDEBSAIIICDQLLEBGSVTMCRNIIQ	540	
Db	481	KKIAFLPMAGCCPLNRPQVLYPLYSLSTPDEBSAIIICDQLLEBGSVTMCRNIIQ	540	

QY 541 QLNQVFLIDYKEICSIPOVIGRLIQNHLSRTCLLAVRTNRARDIRRYLETLEIK 600
 Db 541 QLNQVFLIDYKEICSIPOVIGRLIQNHLSRTCLLAVRTNRARDIRRYLETLEIK 600
 QY 601 APPFYNTVCLIRKLPSHNNTRLRKEMVYFGKNSLOKIOCTPLFAAICAHFQYPPDS 660
 Db 601 APPFYNTVCLIRKLPSHNNTRLRKEMVYFGKNSLOKIOCTPLFAAICAHFQYPPDS 660
 QY 661 FDDVAVFKSYMERLSLRKATBELIKATVSSCEBLAKGPFSCCEFNDDLAEGYDED 720
 Db 661 FDDVAVFKSYMERLSLRKATBELIKATVSSCEBLAKGPFSCCEFNDDLAEGYDED 720
 QY 721 EDITLCLMSKFTAORLPFRFPLSPARQEFLLAGRLIELDSDROHODLALYKQINS 780
 Db 721 EDITLCLMSKFTAORLPFRFPLSPARQEFLLAGRLIELDSDROHODLALYKQINS 780
 QY 781 PMMTVAAYNNFLANYVSSLPSTKAGPKIVSHLHLNDKSELENSENDYIKQPEISIQ 840
 Db 781 PMMTVAAYNNFLANYVSSLPSTKAGPKIVSHLHLNDKSELENSENDYIKQPEISIQ 840
 QY 841 MOLLGLMWCIPQAVFVMSVSEHLVLAALKTAVOSNTVAACSPVLOFLOGRITLTGALNL 900
 Db 841 MOLLGLMWCIPQAVFVMSVSEHLVLAALKTAVOSNTVAACSPVLOFLOGRITLTGALNL 900
 QY 901 QYFDPHPSLSLRSIHPIRGNKTSPPRAHFSVLFTCPDKSOVPTIDODYASAPFPMNW 960
 Db 901 QYFDPHPSLSLRSIHPIRGNKTSPPRAHFSVLFTCPDKSOVPTIDODYASAPFPMNW 960
 QY 961 ERNLAEKEDNVKSYMDOQRASPDLSGTGYKLSPRQYKIPCLFVDVNDIDVGOQMLEIL 1020
 Db 961 ERNLAEKEDNVKSYMDOQRASPDLSGTGYKLSPRQYKIPCLFVDVNDIDVGOQMLEIL 1020
 QY 1021 MTVSASORIELHLNRSRGIESIRPALBELSKASVTKCSISKELSAACQELILTPSLR 1080
 Db 1021 MTVSASORIELHLNRSRGIESIRPALBELSKASVTKCSISKELSAACQELILTPSLR 1080
 QY 1081 SLEVSGTIGSQDQIPFNLDPKFLCLAKELSVDEGNINVFVSIPEEPFPHMEKLLIQISA 1140
 Db 1081 SLEVSGTIGSQDQIPFNLDPKFLCLAKELSVDEGNINVFVSIPEEPFPHMEKLLIQISA 1140
 QY 1141 EYDPSKLVLKILQNSPRLHYFHLKCNFSDRGSLLTMLVSKKLTBIKFSDFFOAVPEVA 1200
 Db 1141 EYDPSKLVLKILQNSPRLHYFHLKCNFSDRGSLLTMLVSKKLTBIKFSDFFOAVPEVA 1200
 QY 1201 SLENFISILKILMEGQPPDEBTSKFAVILGSLNLEBELIPTDGIYRVAKLIIOCCQ 1260
 Db 1201 SLENFISILKILMEGQPPDEBTSKFAVILGSLNLEBELIPTDGIYRVAKLIIOCCQ 1260
 QY 1261 QHAGCLRVLSFFKTLNDDSVVEI 1282
 Db 1261 QHAGCLRVLSFFKTLNDDSVVEI 1282

RESULT 9
 AAM20033
 ID AAM20033 standard; Protein: 1403 AA.
 AC AAM20033;
 XX
 DT 06-OCT-1997 (first entry)
 XX
 DE Neuronal apoptosis inhibitor protein (NAIP).
 KW Neuronal apoptosis inhibitor protein; NAIP; diagnosis;
 KM therapy; cancer; AIDS; amyotrophic lateral sclerosis;
 XX spinal muscular atrophy.
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 600 /note= "encoded by AAA"

FT Misc-difference 919 /note= "encoded by CCA"
 FT
 PN W09726331-A2.
 XX
 XX 24-JUL-1997.
 PD
 XX
 PF 17-JAN-1997; 97MO-IB00142.
 XX
 PR 19-JAN-1996; 96GB-0001108.
 XX
 PA (UYOT-) UNIV OTTAWA.
 PI Korneiluk RG, Mackenzie AE, Robertson G, Roy N, Tamai K;
 DR MPI; 1997-385335/35.
 DR N-PSDB; AAT71266.
 XX
 PT New neuronal inhibitor of apoptosis - useful for diagnosing and
 PT treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis
 PS Claim 41; Fig 7A-L; 102pp; English.

Sequence 1403 AA:
 SQ
 Query Match 77 3%; Score 1084; DB 18; Length 1403;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATOQASDERISQFNDHLPELSALLGLDAVQALKEEEROKERAMQKGVNSQMRSE 60
 Db 1 MATOQASDERISQFNDHLPELSALLGLDAVQALKEEEROKERAMQKGVNSQMRSE 60
 QY 61 AKRLTFVTPYPSYSWIPQEMAAAGFTGVNSGIQCCCSLIFGAGLTRLEPDHAKP 120
 Db 61 AKRLTFVTPYPSYSWIPQEMAAAGFTGVNSGIQCCCSLIFGAGLTRLEPDHAKP 120
 QY 121 HPDGFLLNKDVGNIAYDRIYVNLKSLRGSKMYOBEARLASFRNMPFYVQGISPCV 180
 Db 121 HPDGFLLNKDVGNIAYDRIYVNLKSLRGSKMYOBEARLASFRNMPFYVQGISPCV 180
 QY 181 LSEAGFVFTGKQDVTQCFSCGGLGNWEGDDPMKNAKMPKCEFLRSKXSEETIOT 240
 Db 181 LSEAGFVFTGKQDVTQCFSCGGLGNWEGDDPMKNAKMPKCEFLRSKXSEETIOT 240
 QY 241 QSYKGFVDIGEHFVNSWQRELPMASAYCNDSTIFAYEELRLDSFKDMRRESAVGAA 300
 Db 241 QSYKGFVDIGEHFVNSWQRELPMASAYCNDSTIFAYEELRLDSFKDMRRESAVGAA 300
 QY 301 KAGLFYTGIDTYQCSGCGCLEKNOEGDDPLDHTRCFNPCLFONMKSSAEVTPDIOS 360
 Db 301 KAGLFYTGIDTYQCSGCGCLEKNOEGDDPLDHTRCFNPCLFONMKSSAEVTPDIOS 360
 QY 361 RGEICELLETTSNSLSDSIAGVPIPEMAQSGAKMFOAKNLNQLAAATTSAPFRMS 420
 Db 361 RGEICELLETTSNSLSDSIAGVPIPEMAQSGAKMFOAKNLNQLAAATTSAPFRMS 420
 QY 421 LLDISSDLATDHLACDLSISKISKPVOEPLVLPDEVGNINSVMCVGEAGSGKTVLL 480
 Db 421 LLDISSDLATDHLACDLSISKISKPVOEPLVLPDEVGNINSVMCVGEAGSGKTVLL 480


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OY 481 KKTAPLMAAGCCGCLNRPOLVFLVSLSSRPEGLASTICCOLLEKESGVTEMCRNIIQ 540
DB 481 KKTAPLMAAGCCGCLNRPOLVFLVSLSSRPEGLASTICCOLLEKESGVTEMCRNIIQ 540
OY 541 QLNKQVFLFLDDYKEICISIPQVIGKLIQKNHLSRTCLLIIVATNRADIRRYLETILEIK 600
DB 541 QLNKQVFLFLDDYKEICISIPQVIGKLIQKNHLSRTCLLIIVATNRADIRRYLETILEIK 600
OY 601 APPRYNVICLRLEFHMNTRLKEMVYRGKNSIOXIOKPLVVALICAMPOYPDPDS 660
DB 601 APPRYNVICLRLEFHMNTRLKEMVYRGKNSIOXIOKPLVVALICAMPOYPDPDS 660
OY 661 FDDVAEKSVMERLSLRNKAETELKATVSSCGEIALKGFFSCCFEPNDULAEAGVED 720
DB 661 FDDVAEKSVMERLSLRNKAETELKATVSSCGEIALKGFFSCCFEPNDULAEAGVED 720
OY 721 EDLTMCLMSFTQRIKRPYRPLSPAFQFLAGMLIILLDSQDEHODGCHYHKOINS 780
DB 721 EDLTMCLMSFTQRIKRPYRPLSPAFQFLAGMLIILLDSQDEHODGCHYHKOINS 780
OY 781 PMMTVSAHYNNFLNVSLSPTVAGPKIVSHLLHLDVNKESLENISENDYIKHQPEISIQ 840
DB 781 PMMTVSAHYNNFLNVSLSPTVAGPKIVSHLLHLDVNKESLENISENDYIKHQPEISIQ 840
OY 841 MOLIRGLMOJCPOAYFSVMSEHLVLALKTAVQSTVAAACSPVLOQLQGRITLGLALN 900
DB 841 MOLIRGLMOJCPOAYFSVMSEHLVLALKTAVQSTVAAACSPVLOQLQGRITLGLALN 900
OY 901 QYFPHDESLSLRSIHFPRIKNTSPRAHFSVLETCFQKQVPTIDODVSAFEPNEM 960
DB 901 QYFPHDESLSLRSIHFPRIKNTSPRAHFSVLETCFQKQVPTIDODVSAFEPNEM 960
OY 961 ERNLAEDENVKSYMOMORASPDLSGTWKLSPKOYKIPCLEVDVNDIDVVGQDMLEIL 1020
DB 961 ERNLAEDENVKSYMOMORASPDLSGTWKLSPKOYKIPCLEVDVNDIDVVGQDMLEIL 1020
OY 1021 MTVFSASQRIELHNLNHRGFIESIRPALELSASVATKCSISKLELSAEOELILLTPSLE 1080
DB 1021 MTVFSASQRIELHNLNHRGFIESIRPALELSASVATKCSISKLELSAEOELILLTPSLE 1080
OY 1081 SLEVSQITQSDODIPRLDKFCLKELSDLEGNINVSVPPEEPNHNHEKLLIOISA 1140
DB 1081 SLEVSQITQSDODIPRLDKFCLKELSDLEGNINVSVPPEEPNHNHEKLLIOISA 1140
OY 1141 EYDSKLVKLIQNSPNLHVFHLKCNFFSDGSLMTMLVSCCKLLEIKFSDFFOAVFVA 1200
DB 1141 EYDSKLVKLIQNSPNLHVFHLKCNFFSDGSLMTMLVSCCKLLEIKFSDFFOAVFVA 1200
OY 1201 SLPNFIKLTINLBGOQFPDEETSEKFAVILGSLNLEBLLIPTGDDGIYRAKLIIOCCQ 1260
DB 1201 SLPNFIKLTINLBGOQFPDEETSEKFAVILGSLNLEBLLIPTGDDGIYRAKLIIOCCQ 1260
OY 1261 QLHCLRVLSFFKTLNDSVVEIAKVA 1286
DB 1261 QLHCLRVLSFFKTLNDSVVEIAKVA 1286

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RESULT 10

AAR98217 AAR98217 standard; Protein; 1232 AA.

AAR98217;

30-DEC-1996 (first entry)

Neuronal apoptosis inhibiting protein.

Neuronal apoptosis inhibiting protein; human; NAIp; chromosome 5q13; YAC;

Yeast artificial chromosome; spinal muscular atrophy; mammalian cell;

autosomal recessive; neurodegenerative disorder; alpha motor neuron; SMA;

spinal cord; proximal voluntary muscle; therapy; apoptotic mechanism.

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OS Homo sapiens.
XX W09612016-A1.
XX 25-APR-1996.
XX 17-OCT-1995; 95MO-CA00581.
XX 19-DEC-1994; 94CA-2138425.
XX 18-OCT-1994; 94GB-0021019.
XX (SHKJ) RES DEV CORP JAPAN.
XX (UYOT-) UNIV OTTAWA.
XX Ikeda J, Korneluk RG, Mackenzie AE, Mahadevan MS;
XX Mclean M, Roy N;
XX MPI: 1996-222003/22.
XX N-PSDB; AAT30092.
XX Claim 3; Page 68-70; 113pp; English.
XX This sequence represents the human neuronal apoptosis inhibitor protein
XX (NAIp). The cDNA encoding this sequence was found on a region of the
XX human chromosome 5q13. This sequence was isolated from a yeast
XX artificial chromosome (YAC) contig containing the D5S435-D5S112 interval
XX of the chromosome 5q13. Mutations in the NAIp gene, are causative of
XX spinal muscular atrophy (SMA) types I, II, and III. SMAs are a group of
XX autosomal recessive, neurodegenerative disorders. SMAs are classified
XX into three types based upon the age of onset (with type I being the
XX severest form with the earliest age of onset). All three types are
XX characterised by the degeneration of the alpha motor neurons of the
XX spinal cord manifesting as weakness and wasting of the proximal voluntary
XX muscles. The most common mutations of the NAIp gene sequence are thought
XX to be deletions of exons 5 and 6, and reductions in the copy number of
XX the gene. The NAIp gene, (and primers and probes based on it) can be
XX used for the diagnosis of SMA, and for directing the formulation of
XX conventional and genetic therapies for SMA. Identification of genes
XX showing homology with the NAIp locus, and proteins that interact with
XX NAIp can be used in the elucidation of apoptotic mechanisms in mammalian
XX cells.
SQ Sequence 1232 AA:
Query Match 67.4%; Score 946; DB 17; Length 1232;
Best Local Similarity 99.8%; Pred No 0;
Matches 1146; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 MATOQKASDERISQPHNLLPRLSALLGLDAVOLAKSLBEEBOKERAKMOGVNSQMRSE 60
DB 1 MATOQKASDERISQPHNLLPRLSALLGLDAVOLAKSLBEEBOKERAKMOGVNSQMRSE 60
OY 61 AKRLKFTVTEPEPSSWIPQMAAGFPYGVSGIQCCGSLIFGAGLTRLPEDHKRF 120
DB 61 AKRLKFTVTEPEPSSWIPQMAAGFPYGVSGIQCCGSLIFGAGLTRLPEDHKRF 120
OY 61 AKRLKFTVTEPEPSSWIPQMAAGFPYGVSGIQCCGSLIFGAGLTRLPEDHKRF 120
DB 61 AKRLKFTVTEPEPSSWIPQMAAGFPYGVSGIQCCGSLIFGAGLTRLPEDHKRF 120
OY 121 HPDGGFLANDVGNIAKYDIRVKNLSKRLGGKMYOBBEARLASFRNWPYVGISPCV 180
DB 121 HPDGGFLANDVGNIAKYDIRVKNLSKRLGGKMYOBBEARLASFRNWPYVGISPCV 180
OY 121 HPDGGFLANDVGNIAKYDIRVKNLSKRLGGKMYOBBEARLASFRNWPYVGISPCV 180
DB 121 HPDGGFLANDVGNIAKYDIRVKNLSKRLGGKMYOBBEARLASFRNWPYVGISPCV 180
OY 181 LSEAGFVFTGKQDTPVCFSCGCGCLGMBEGDDPMKEHAKMPKCEPLRSKSSSRITQYI 240
DB 181 LSEAGFVFTGKQDTPVCFSCGCGCLGMBEGDDPMKEHAKMPKCEPLRSKSSSRITQYI 240
OY 181 LSEAGFVFTGKQDTPVCFSCGCGCLGMBEGDDPMKEHAKMPKCEPLRSKSSSRITQYI 240
DB 181 LSEAGFVFTGKQDTPVCFSCGCGCLGMBEGDDPMKEHAKMPKCEPLRSKSSSRITQYI 240
OY 241 QSYKGFVDITGEHFNVSQVRLPMAASAYCNDISFAYEBLRLDSFKMPRESAGVAAALA 300
DB 241 QSYKGFVDITGEHFNVSQVRLPMAASAYCNDISFAYEBLRLDSFKMPRESAGVAAALA 300
OY 301 KAGGFYTGIDIVQCSGCGCLEKMOBGDDPLDDITRQFPCPCFLQNNKSSABVTPLQSS 360
DB 301 KAGGFYTGIDIVQCSGCGCLEKMOBGDDPLDDITRQFPCPCFLQNNKSSABVTPLQSS 360

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Db      301 KAGLFYTGIDIVOCFSCCGCIEKMEQSDPDLDRTRCFENCFPLQNMKRSAAEVTPLDLS 360
Qy      361 RGEICELLETTESNTEDSIAGVPTPEMAQGEAOMQEAONLEOLRAAYTASAFRMS 420
Db      361 RGEICELLETTESNTEDSIAGVPTPEMAQGEAOMQEAONLEOLRAAYTASAFRMS 420
Qy      421 LDDISSDLATDHLGCDLSIASKHSKRPVQEPVLPRVPCNLNSVWCVEGEGSGKTVLL 480
Db      421 LDDISSDLATDHLGCDLSIASKHSKRPVQEPVLPRVPCNLNSVWCVEGEGSGKTVLL 480
Qy      481 KKIAFLMAGSCCPLNRPQVYLSISTSTRPDGLASII CDLLEKESVTENCMRNIIQ 540
Db      481 KKIAFLMAGSCCPLNRPQVYLSISTSTRPDGLASII CDLLEKESVTENCMRNIIQ 540
Qy      541 QLNQVULPLDDYKEICSIPOVIGKLIQKNHLSRTCLIAVTRNARIRIYETLTLEIK 600
Db      541 QLNQVULPLDDYKEICSIPOVIGKLIQKNHLSRTCLIAVTRNARIRIYETLTLEIK 600
Qy      601 APPFNTVCILRKLFSSHMTRLKRFMYRGKNSLOKOTPLFVAACAHMFQYFPDPS 660
Db      601 APPFNTVCILRKLFSSHMTRLKRFMYRGKNSLOKOTPLFVAACAHMFQYFPDPS 660
Qy      661 PDDVAVFSYMERLSLANKATATILKATVSSCGELALGFPSCCFEENDDDLAAGVDD 720
Db      661 PDDVAVFSYMERLSLANKATATILKATVSSCGELALGFPSCCFEENDDDLAAGVDD 720
Qy      721 EBLTMCMSKFTQAORLAPFYRFLSPAFOEFLAGMLIELLSDRQEHQDLGLVHLKQNS 780
Db      721 EBLTMCMSKFTQAORLAPFYRFLSPAFOEFLAGMLIELLSDRQEHQDLGLVHLKQNS 780
Qy      781 PMNTVASANNFLNVSSLPSTKAGPRTVSHLHLVDNKESENISENDYLRKQPRISIQ 840
Db      781 PMNTVASANNFLNVSSLPSTKAGPRTVSHLHLVDNKESENISENDYLRKQPRISIQ 840
Qy      841 MQLLRGKMOICPAYFSMSYSEHLVLAALKTAQNTVAACSPVLOFLOGRTLTGALNL 900
Db      841 MQLLRGKMOICPAYFSMSYSEHLVLAALKTAQNTVAACSPVLOFLOGRTLTGALNL 900
Qy      901 QYFPHDEBSILSLRSHIPRGNKTSPPRAHFSVLETCFDSQVPTIDDOYAAAFPMNEM 960
Db      901 QYFPHDEBSILSLRSHIPRGNKTSPPRAHFSVLETCFDSQVPTIDDOYAAAFPMNEM 960
Qy      961 ERNLAEKEDNVKSYNDMORRASPDLSTGYMKLSKQYKPCLEVDNDIDVGDMLIEL 1020
Db      961 ERNLAEKEDNVKSYNDMORRASPDLSTGYMKLSKQYKPCLEVDNDIDVGDMLIEL 1020
Qy      1021 MTFVSAOSRIEHLNHSQFTESIRPALFELSKASYTKCSISKLELSAAEQELLTLPSLE 1080
Db      1021 MTFVSAOSRIEHLNHSQFTESIRPALFELSKASYTKCSISKLELSAAEQELLTLPSLE 1080
Qy      1081 SLEVSCTIQSODQIFPNLDFLCKELSYVDLEGNIVFVTEEPENHHEKLLIOTISA 1140
Db      1081 SLEVSCTIQSODQIFPNLDFLCKELSYVDLEGNIVFVTEEPENHHEKLLIOTISA 1140
Qy      1141 EYDPSKLV 1148
Db      1141 EYDPSKLV 1148

```

RESULT 11
AAB53493 standard; Protein; 118 AA.

AA 09-MAR-2001 (first entry)
Human colon cancer antigen protein sequence SEQ ID NO:1033.
Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytotoxic; cardiotoxic; neuroprotective; vulnerary; immunomodulatory; muscular; gynecological; gastrointestinal; nephrotropic; anti-infective; antibacterial; gene therapy; wound;

KM neural disorder; immune system disorder; muscular disorder;
KM reproductive disorder; gastrointestinal disorder; renal disorder;
KM infectious disease; cardiovascular disorder.
XX
OS Homo sapiens.
PN WO20005351-A1.
XX
PD 21-SEP-2000.
XX
PE 08-MAR-2000; 2000MO-US05883.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Ruben SM;
XX
DR WPI: 2000-58734/55.
DR N-PSDB; AAC98250.
XX
PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
XX disorders such as colon cancer.
XX
PS Claim 11; Page 1612; 2104pp; English.
XX
CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytotoxic, cardiotoxic, muscular;
CC neuroprotective, immunomodulatory, gynecological, gastrointestinal, muscular;
CC vulnerary, nephrotropic, anti-infective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridization probes. The proteins
CC may also be used to prevent diseases such as neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders, infectious
CC gastrointestinal disorders, wounds, renal disorders, infectious
CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
CC AAC98773 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 118 AA;
Query Match 5.3%; Score 75; DB 21; Length 118;
Best Local Similarity 100.0%; Pred. No. 6,3e-69;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 607 TYCIRKLFSSHMTRLKRFMYRGKNSLOKOTPLFVAACAHMFQYFPDPSFDDVAV 666
Db 1 TYCIRKLFSSHMTRLKRFMYRGKNSLOKOTPLFVAACAHMFQYFPDPSFDDVAV 60
Qy 667 FKSYMERLSLNKAT 681
Db 61 FKSYMERLSLNKAT 75

RESULT 12
AAG01849 standard; Protein; 60 AA.

AA 06-OCT-2000 (first entry)
Human secreted protein, SEQ ID NO: 5930.
Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
XX
OS Homo sapiens.

XX PA EPI033401-A2.
XX XX
XX PD 06-SEP-2000.
XX XX
XX PF 21-FEB-2000; 2000EP-0200610.
XX XX
XX PT 26-FEB-1999; 99US-0122487.
XX XX
XX (GEST) GENSET.
XX PA
XX PI Dumas Milne Edwards J, Duclet A, Giordano J;
XX WPI; 2000-500381/45.
XX DR N-PSDB; AAC01855.
XX XX
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX PS
XX Claim 13; SEQ ID 5930; 71bp + CD-ROM; English.
XX CC The present sequence is a polypeptide encoded by one of a large number
XX CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
XX CC were prepared from total human RNAs or polyA+ RNAs derived from 30
XX CC different tissues. EST sequences usually correspond mainly to the 3'
XX CC untranslated region (UTR) of the mRNA because they are often obtained
XX CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
XX CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
XX CC those cases where longer cDNA sequences have been obtained, the full 5'
XX CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
XX CC ends and can therefore be used to obtain full length cDNAs and genomic
XX CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
XX CC chromosome mapping procedures. They are used to obtain upstream
XX CC regulatory sequences and to design expression and secretion vectors.
XX SQ
XX Sequence 60 AA;
XX
XX Query Match 4.3%; Score 60; DB 21; Length 60;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-53;
XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 265 MASAYCNDISFAYEBELRDSFKDMPRESAVGVAALAKKGLFTGTGKDIYOCFSGCGLKX 344
XX DB 1 MASAYCNDISFAYEBELRDSFKDMPRESAVGVAALAKKGLFTGTGKDIYOCFSGCGLKX 60
XX
XX RESULT 13
XX ID AA012411 standard; Protein; 51 AA.
XX AC AA012411;
XX XX
XX DT 06-NOV-2001 (first entry)
XX XX
XX DE Human polypeptide SEQ ID NO 26303.
XX XX
XX KM Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KM tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KM nervous system disorders; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200164835-A2.
XX XX
XX PD 07-SEP-2001.
XX XX
XX PF 26-FEB-2001; 2001MO-US04927.
XX XX
XX PR 28-FEB-2000; 2000US-0515126.
XX PR 18-MAY-2000; 2000US-0577409.
XX XX

XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Dymnac RT;
XX XX
XX DR WPI; 2001-514838/56.
XX N-PSDB; AA192342.
XX XX
XX PT Isolated nucleic acids and polypeptides, useful for preventing
XX PT diagnosing and treating e.g. leukaemia, inflammation and immune
XX PT disorders -
XX PS
XX Claim 20; SEQ ID NO 26303; 1399bp + Sequence listing; English.
XX XX
XX CC The invention relates to human polynucleotides (AA179941-AA193841) and
XX CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
XX CC cytokine, cell proliferation or cell differentiation or which may induce
XX CC production of other cytokines in other cell populations. The
XX CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX CC peptide therapy. The polypeptides have various cytokine-like activities,
XX CC e.g. stem cell growth factor activity, haematopoiesis regulating
XX CC activity, tissue growth factor activity, immunomodulatory activity and
XX CC activin/inhibin activity and may be useful in the diagnosis and/or
XX CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX CC inflammation.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ
XX Sequence 51 AA;
XX
XX Query Match 1.8%; Score 25; DB 22; Length 51;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-17;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 224 CEPLRSKKSSEETITOTYISYKGFVD 248
XX DB 10 CEPLRSKKSSEETITOTYISYKGFVD 34
XX
XX RESULT 14
XX ID ABG55972 standard; Peptide; 37 AA.
XX AC ABG55972;
XX XX
XX DT 25-FEB-2003 (first entry)
XX XX
XX DE Human liver peptide, SEQ ID NO 34620.
XX XX
XX KM Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX KM hypercholesterolaemia; coronary heart disease.
XX OS Homo sapiens.
XX PN WO200157273-A2.
XX XX
XX PD 09-AUG-2001.
XX XX
XX PF 30-JAN-2001; 2001MO-US00664.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX XX

XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human adult liver -
 XX
 XX Claim 27; SEQ ID No 34620; 658bp; English.
 CC The invention relates to a single exon nucleic acid probe (SENP) (1) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridizes at high
 CC stringency to a nucleic acid molecule expressed in the human adult
 CC liver. (1) may be used for predicting, measuring and displaying gene
 CC expression in samples derived from human adult liver. The genes
 CC identified may be involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinemia, hyperlipidaemia and hypercholesterolemia which
 CC is associated with coronary heart disease. AB547348-AB559310 represent
 CC human liver single exon encoded peptides of the invention.
 CC Note: The sequence information for this patent does not appear in the
 CC printed specification but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 37 AA;

Query Match 1.6%; Score 22; DB 22; Length 37;
 Best Local Similarity 100.0%; Pred. No. 2,4e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 229 SKKSEBITIYIOSYKGFVDIT 250
 DB 1 SKKSEBITIYIOSYKGFVDIT 22

RESULT 15
 ID AAM74180 standard; Protein; 37 AA.
 AC AAM74180;
 DT 06-NOV-2001 (first entry)
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34486.
 XX Human; bone marrow expressed exon; gene expression analysis; probe;
 KM microarray; cancer; leukemia; lymphoma; myeloma.
 XX Homo sapiens.
 OS WO200157276-A2.
 PN 30-JAN-2001; 2001WO-US00668.
 PD 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00668.
 PF 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR,
 XX
 XX WPI; 2001-488900/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human bone marrow -
 XX
 XX Example 4; SEQ ID NO: 34486; 658bp + Sequence Listing; English.
 PS The present invention provides a number of single exon nucleic acid
 CC

CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.
 CC
 SQ Sequence 37 AA;

Query Match 1.6%; Score 22; DB 22; Length 37;
 Best Local Similarity 100.0%; Pred. No. 2,4e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 229 SKKSEBITIYIOSYKGFVDIT 250
 DB 1 SKKSEBITIYIOSYKGFVDIT 22

RESULT 16
 ID AAM34307 standard; Protein; 37 AA.
 AC AAM34307;
 DT 17-OCT-2001 (first entry)
 DE Peptide #8344 encoded by probe for measuring placental gene expression.
 XX Probe; microarray; human; placenta; antenatal diagnosis;
 KM genetic disorder.
 XX
 OS Homo sapiens.
 OS WO200157272-A2.
 PN 09-AUG-2001.
 PD 30-JAN-2001; 2001WO-US00663.
 PF 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR,
 XX
 XX WPI; 2001-488900/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human placenta -
 XX
 XX Claim 27; SEQ ID No 34576; 654bp; English.
 CC The present invention relates to single exon nucleic acid probes (SENP;
 CC see AAI1315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.
 CC
 SQ Sequence 37 AA;

Query Match 1.6%; Score 22; DB 22; Length 37;
 Best Local Similarity 100.0%; Pred. No. 2,4e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 229 SKKSEBITIYIOSYKGFVDIT 250
 DB 1 SKKSEBITIYIOSYKGFVDIT 22

RESULT 17
ABG44119
ID ABG44119 standard; Peptide; 37 AA.
XX
XX ABG44119;
DT 19-AUG-2002 (first entry)
XX
DB Human peptide encoded by genome-derived single exon probe SEQ ID 33784.
XX
XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease.
XX
XX Homo sapiens.
XX
XX MO200186003-A2.
XX
PD 15-NOV-2001.
XX
PP 30-JAN-2001; 2001MO-US00665.
XX
PR 04-FEB-2000; 2000US-180312P.
PR 26-MAY-2000; 2000US-207456P.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-063236P.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
DT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
XX Claim 27; SEQ ID NO 33784; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of
XX probes; the novel set of probes which hybridise at high stringency to a
XX nucleic acid expressed in the human lung; measuring gene expression to a
XX sample derived from human lung, comprising (a) contacting the array with
XX a collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of
XX the array; identifying exons in a eukaryotic genome, comprising
XX (a) algorithmically predicting at least one exon from genomic sequences
XX of the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryotic lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the

CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a peptide/protein
CC encoded by a single exon probe of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 37 AA;
SQ
Query Match 1.6%; Score 22; DB 23; Length 37;
Best Local Similarity 100.0%; Pred. No. 2,4e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 229 SKKSEETQYIOSYKGFVDIT 250
DB 1 SKKSEETQYIOSYKGFVDIT 22
RESULT 18
AA065778
ID AA065778 standard; Protein; 67 AA.
XX
XX AA065778;
XX
DT 06-NOV-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 20670.
DE
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001MO-US04927.
XX
XX 28-FEB-2000; 2000US-0515126.
XX
XX 18-MAY-2000; 2000US-0577409.
XX
XX (HYSB-) HYSB INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-514838/56.
XX
XX N-PSDB; AA186709.
XX
DT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
XX disorders -
XX
XX Claim 20; SEQ ID NO 20670; 1399pp + Sequence listing; English.
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
XX the encoded proteins (AA000010-AA013910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC XX

SO Sequence 67 AA;

Query Match 0.64; Score 9; DB 22; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1377 MKERHPSK 1385
 |||||
 Db 41 MKERHPSK 49

RESULT 19
 ABP81447
 ID ABP81447 standard; Protein; 210 AA.
 XX
 AC ABP81447;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE Streptococcus pneumoniae polypeptide SEQ ID NO 364.
 XX
 KW Streptococcus pneumoniae; infection; otitis media; antibacterial;
 XX diagnosis; gene therapy.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN WO200283855-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 12-APR-2002; 2002WO-US11524.
 XX
 PR 16-APR-2001; 2001US-283948P.
 XX
 PR 18-APR-2001; 2001US-284443P.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Zagursky RJ, Maei AW, Green BA, Chakravarti DN, Russell DP;
 XX Woelke RJ;
 XX
 WIPI; 2003-093010/08.
 DR N-PSDB; AB242295.
 DR
 XX
 PT New Streptococcus pneumoniae polynucleotides, useful for treating or
 PT preventing S. pneumoniae infections, or non-systemic diseases, e.g.,
 PT otitis media, which are induced or exacerbated by S. pneumoniae -
 XX
 PS Claim 42, Page 599-600; 1091pp; English.

CC The invention relates to isolated polynucleotides (AB272147-AB242522) of
 CC a Streptococcus pneumoniae genomic sequence, a fragment or degenerate
 CC variant of the polynucleotide or a nucleic acid sequence 95% identical to
 CC one of the polynucleotides. The S. pneumoniae polynucleotides and
 CC encoded polypeptides (ABP81299-ABP81674) are useful for treating or
 CC preventing S. pneumoniae infections or non-systemic diseases, e.g., otitis
 CC media, which are induced or exacerbated by S. pneumoniae. These are also
 CC useful for detecting S. pneumoniae in a biological sample or diagnosing
 CC S. pneumoniae infection in a subject. The polynucleotides have
 CC antibacterial activity and are useful in gene therapy.
 CC
 CC Sequence 210 AA;

Query Match 0.64; Score 9; DB 24; Length 210;
 Best Local Similarity 100.0%; Pred. No. 4.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 473 GSGKTVLLK 481
 |||||
 Db 38 GSGKTVLLK 46

RESULT 20
 AB002180
 ID AB002180 standard; Protein; 210 AA.
 XX
 AC AB002180;
 XX
 DT 11-FEB-2003 (first entry)
 XX
 DE 5. pneumoniae type 4 strain protein from coding region #1757.
 XX
 KW Bacterial meningitis; pneumonia; sepsis; otitis media;
 KW ear infection; antiinflammatory; antibacterial; immunostimulant;
 XX auditory; respiratory; gene therapy; vaccine.
 XX
 OS Streptococcus pneumoniae type 4 strain.
 XX
 PN WO200277021-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 27-MAR-2002; 2002WO-1802163.
 XX
 PR 27-MAR-2001; 2001GB-0007658.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Maignant V, Tettelin H, Frazer C;
 XX
 WIPI; 2003-040579/03.
 DR N-PSDB; ABX07469.
 DR
 XX
 PT New proteins and nucleic acid molecules from Streptococcus pneumoniae,
 PT useful as medicaments for treating or preventing a disease or infection
 PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
 PT or ear infection -
 XX
 PS Claim 1, SEQ ID No 3514; 56pp; English.

CC The invention relates to a protein comprising or having at least 50%
 CC identity to any of the 2469 amino acid sequences, identified in the
 CC specification (available on a computer readable format), or its fragment,
 CC expressed from 2469 of 2489 identified DNA coding regions from the
 CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
 CC AB556454. Also included are an antibody which binds one of the
 CC proteins, treating a patient by administering the protein, DNA or
 CC antibody (in a composition), a kit comprising first and second primers,
 CC which are the nucleic acid cited above or fragments between nucleotides
 CC 8-100 of a sequence contained within the specification, for amplifying a
 CC target sequence contained within a Streptococcus nucleic acid sequence,
 CC where the first primer is substantially complementary to the target
 CC sequence and the second primer is substantially complementary to the
 CC complement of the target sequence, and where the pairs of the primers
 CC having substantial complementarity define the termini of the target
 CC sequence to be amplified, assay comprising contacting a test compound
 CC with the protein, and determining whether the test compound binds to the
 CC protein and a Streptococcus pneumoniae bacterium, where one or more
 CC genes encoding the proteins has been rendered inactive. The proteins,
 CC nucleic acid molecules, antibody and compositions are useful as
 CC medicaments for treating or preventing a disease or infection due to
 CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia,
 CC sepsis, otitis media or ear infection. They are also useful in developing
 CC vaccines, diagnostics and antibiotics. The methods are useful for
 CC identifying immunodominant proteins. The present sequence is one of
 CC the 2469 proteins expressed by the identified coding regions from the
 CC genomic sequence.

CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pat_sequences.

SQ Sequence 210 AA;

Query Match	0.6%	Score 9;	DB 24;	Length 210;
Best Local Similarity	100.0%	Pred. No. 4.1;		
Matches	9;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY 473 GSGKTVLLK 481

Db 38 GSGKTVLLK 46

RESULT 21

ID AAG28074 standard; Protein; 341 AA.

AC AAG28074;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 33155.

KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter
KM termination sequence.

OS *Arabidopsis thaliana*.

PN BP1033405-A2

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439

PR	25-FEB-1999	99US-0121825
PR	03-MAR-1999	99US-0123348
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PR 05-AUG-1999; 99US-0147192.
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PR 01-SEP-1999; 99US-0151930.
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PR 26-OCT-1999; 99US-0161360.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 0.6%; Score 9; DB 22; Length 349;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 LAKSLEEBE 42
Db 95 LAKSLEEBE 103

RESULT 22
AAB65694
ID AAB65694 standard; Protein; 349 AA.
XX
AC AAB65694;
XX
DT 27-MAR-2001 (first entry)
XX
DE Novel protein kinase, SEQ ID NO: 222.
XX
KW Human; mouse; protein kinase; antihypertic; antisclerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antidiabetic;
KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX
OS Mus musculus.
XX
PN WO200073469-A2.
XX
PD 07-DEC-2000.
XX
PE 26-MAY-2000; 2000NO-US14842.
XX
PR 28-MAY-1999; 99US-0136503.
XX
PA (SUGEN-) SUGEN INC.
XX
PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX
DR WPI; 2001-032161/04.
XX
DR N-PSDB; AAF44722.
XX
PT Nucleic acid encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers -
XX
PS Claim 10; Fig 1; 310p; English.
XX
CC The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure,
CC oxidative-stress related disorders, chronic inflammatory bowel disease,
CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
CC reproductive disorders.
XX
SQ Sequence 349 AA;

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OY 1231 LGSLSNLEE 1239
DB 153 LGSLSNLEE 161

RESULT 23

AAU03542 standard; Protein; 350 AA.

AAU03542;

12-SEP-2001 (first entry)

Human protein kinase #42.

Human; protein kinase; PK; STK; cancer; cardiovascular disease;

metabolic disorder; immune related disease; neurological disorder;

neurodegenerative disorder; inflammatory disorder; infectious disease;

reproductive disorder.

Homo sapiens.

WO200138503-A2.

31-MAY-2001.

22-NOV-2000; 2000MO-US32085.

24-NOV-1999; 99US-0167482.

(SUGC-) SUGEN INC.

Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;

Flanagan P, Clary D;

WPI; 2001-343950/36.

N-PSDB; AAS06742.

Nucleic acids encoding human kinase polypeptides, useful for preventing

diagnosing and/or treating e.g. cancer, immune, cardiovascular and

neural-associated diseases, and microbial infections -

Claim 7; Figure 2; 433pp; English.

AAU03501-AAU03557 represent novel human protein kinases #1-57. The

novel protein kinases have been identified as members of the tyrosine

or serine/threonine kinase (PTK and STK) families. The polynucleotides

encoding protein kinases and the polypeptides may be used in the

prevention, diagnosis and treatment of diseases associated with

inappropriate kinase expression. For example, they may be used to treat

cancers (especially cancers of haematopoietic origin), cardiovascular

disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),

immune related diseases (e.g. rheumatoid arthritis), neurological

disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.

Parkinson's disease), inflammatory disorders (e.g. asthma), infectious

disease (e.g. HIV) and reproductive disorders (e.g. infertility).

Additionaly, polynucleotides encoding protein kinases may be

used for gene therapy and as DNA probes in diagnostic assays.

The protein kinase polypeptides may be used as antigens in the production

of antibodies against the protein kinases and in assays to identify

modulators of protein kinase expression and activity.

Sequence 350 AA;

Query Match 0.6%; Score 9; DB 22; Length 350;

Best Local Similarity 100.0%; Pred. No. 6.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1231 LGSLSNLEE 1239

DB 154 LGSLSNLEE 162

RESULT 24
ABP69792 standard; Protein; 350 AA.

ABP69792;

20-JAN-2003 (first entry)

Human polypeptide SEQ ID NO 1839.

Human; genome mapping; gene therapy; food supplement; virus; fungus;

cell-proliferative disorder; neurodegenerative disease; bacterial;

Parkinson's disease; Alzheimer's disease; autoimmune disease;

multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;

arthritis; cytostatic; immunomodulator; nocotropic; neuroprotective;

antiparkinsonian; antidiabetic; immunosuppressive; dermatological;

haemostatic; vulnerary; fungicide; antibacterial; vituicide; protozoicide;

antithrilitic.

Homo sapiens.

WO200270539-A2.

12-SEP-2002.

05-MAR-2002; 2002MO-US05095.

05-MAR-2001; 2001US-0799451.

(HYSE-) HYSEQ INC.

Tang YT, Zhou P, Goodrich RM, Aundi V, Zhang J, Zhao Q, Ren F;

Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;

Weinman T, Wang J, Wang D, Drmanac RT;

WPI; 2002-759812/82.

N-PSDB; ABZ12009.

New polynucleotides comprising sequences assembled from expressed

sequence tags (BSTs), useful for treating cell-proliferative,

neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or

platelet or coagulation disorders -

Claim 9; SEQ ID NO 1839; 1012pp + Sequence Listing; English.

The invention relates to an isolated polynucleotide (I) comprising a

nucleotide sequence selected from any of 948 sequences

(ABZ1119-ABZ12066) or their mature protein coding portion, active domain

coding protein or complementary sequences. The polynucleotides are useful

for identifying expressed genes or for physical mapping of human genome.

The encoded polypeptides (ABP69902-ABP69949) are useful as molecular

weight markers, as a food supplement, for generating antibodies, in

medical imaging, screening and diagnostic assays and for treating

cell-proliferative disorders (cancer), neurodegenerative diseases

(Parkinson's or Alzheimer's disease), autoimmune diseases (multiple

sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid

disorders, platelet or coagulation disorders, wound, burns, infection,

ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,

parasitic), arthritis, etc.

Note: The sequence data for this patent did not form part of the printed

specification, but was obtained in electronic format directly from WIPO

at ftp.wipo.int/pub/published_pct_sequences.

Sequence 350 AA;

Query Match 0.6%; Score 9; DB 23; Length 350;

Best Local Similarity 100.0%; Pred. No. 6.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1231 LGSLSNLEE 1239

DB 154 LGSLSNLEE 162

RESULT 25
AAG28073
ID AAG28073 standard; Protein; 416 AA.
XX
XX AAG28073;
AC
XX
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33154.
XX
XX Protein identification: signal transduction pathway; metabolic pathway;
KW hydrolase assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
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PR 02-JUL-1999; 99US-0142055.
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XX
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XX hydridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
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XX 25-FEB-2000; 2000EP-0301439.
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PR 27-AUG-1999; 99US-0151065.

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DB 223 LAKELEEE 231

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RESULT 27
AAE17965
ID AAE17965 standard; peptide; 15 AA.
XX
AC AAE17965;
XX
DT 07-MAY-2002 (first entry)
XX
DE Polyoma virus large T-antigen peptide deletion mutant, TMD-25 #7.
XX Human; proliferative disorder; tumor host range mutant virus; cancer;
XX T-HR mutant; Sal2 gene; ovarian tumour; T-antigen; mutant; mutein.
XX

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OS Polyma virus.
OS Synthetic.
XX WO200204596-A2.
XX 17-JAN-2002.
XX 05-JUL-2001; 2001WO-US21354.
XX 07-JUL-2000; 2000US-216723P.
PR 19-MAR-2001; 2001US-0812471.
PR 19-MAR-2001; 2001US-0812633.
XX
XX (HARD) HARVARD COLLEGE.
PA (BGHM) BRIGHAM & WOMEN'S HOSPITAL INC.
PI Benjamin TL, Li D, Mok SC, Cramer DW, Ma Y;
XX WPI; 2002-164637/21.
XX
XX Detecting protein involved in susceptibility to proliferative disease,
PT by infecting normal and abnormal proliferating cells with mutant virus,
PT detecting mutated protein allowing growth of mutant on abnormal cells
PT
XX
XX
XX Example 2; Fig 2C, 92pp; English.
XX The invention relates to a method for the identification of genes
CC and their encoded proteins involved in susceptibility to proliferative
CC disorder, including cancer using a tumor host range mutant (T-HR
CC mutant) virus. The invention also provides the use of Sal2 genes and
CC proteins in methods of identifying a mammal having, or at a risk of
CC acquiring a proliferative disease. T-HR mutants are used to kill cancer
CC cells such as one carrying a Sal2 alteration. Transgenic and knockout
CC mouse comprising Sal2 nucleic acid are useful as research tools to
CC determine genetic and physiological features of cancer and for
CC identifying compounds that can affect ovarian and other tumours. The
CC present sequence is Polyma virus large T-antigen peptide deletion
CC mutant, TMD-25. This peptide is used in the exemplification of the
CC invention.
XX
XX Sequence 15 AA;
SO
Query Match 0.6%; Score 8; DB 23; Length 15;
Best local Similarity 100.0%; Pred.No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 326 QEGDDPUD 333
DB 3 QEGDDPUD 10
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ID AAM83576 standard; Protein; 56 AA.
XX AAM83576;
AC AAM83576;
XX 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen SEQ ID NO:11169.
DE
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW Cytostatic; gene therapy; vaccine; metastasis.
XX Homo sapiens.
OS
XX WO200157182-A2.
XX 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US01354.
XX

PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
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 PR 08-DEC-2000; 2000US-0251858.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251969.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI, 2001-483426/52.
 XX N-PSDB; AAK56357.
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 useful for preventing, diagnosing and/or treating cancers and

PT metastasis -
 XX
 PS Claim 11, SEQ ID NO 11169; 3071pp + Sequence listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK62170 to AAK61921. (I) have cytotoxic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK67694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK62169
 CC represent sequences used in the exemplification of the present invention.
 CC
 SO Sequence 56 AA:

Query Match 0.6%; Score 8; DB 22; Length 56;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 633 QSLQKIQK 640
 DB 40 QSLQKIQK 47

RESULT 29
 ABB50632
 ID ABB50632 standard; Protein; 64 AA.

XX ABB50632;
 DT 07-FEB-2002 (first entry)
 XX
 DE Human secreted protein encoded by gene 36 SEQ ID NO:580.

XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
 KW dermatological; immunosuppressive; anti-inflammatory; immunostimulant;
 KW cytoprotective; cardiac; vascular; anti-angiogenic; ophthalmological;
 KW neuroprotective; anti-tumor; anticonvulsant; antialzheimer's; vulnary;
 KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
 KW Gaucher's disease; cardiovascular disease; Schmitz syndrome; chemoaxis;
 KW Chagas's cardiomyopathy; coronary arteriosclerosis; angio-genic disorder;
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;
 KW Parkinson's disease; infectious disease; Chromosome 14.

XX Homo sapiens.
 OS
 XX WO200162891-A2.
 XX
 PN 30-AUG-2001.
 XX
 PD 21-FEB-2001; 2001WO-US05614.
 XX
 PP 24-FEB-2000; 2000US-184836P.
 PR 29-MAR-2000; 2000US-193170P.
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 XX

PA (HUMA-) HUMAN GENOME SCI INC.
 PI Ni J, Edner R, Lafleur DM, Moore PA, Olsen HS, Rosen CA;
 PI Ruben SM, Soppe DR, Young PE, Shi Y, Florence KA, Wei Y,
 PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Pettie AW, Fan P,
 PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;

PI Zeng Z, Greene JM;
 XX MPI; 2001-625724/72.
 DR
 XX Nucleic acids encoding 207 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX
 XX Disclosure; Page 85; 1533pp; English.
 XX
 CC AAB50301 to AAB51287 and AAB83194 to ABA83441 represent human secreted
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 CC activities based on the tissues and cells the genes are expressed in.
 CC Example of these activities include: immunomodulatory; antisclerotic;
 CC dermatological; immunosuppressive; anti-inflammatory; immunostimulant;
 CC anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological;
 CC neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;
 CC antiparkinsonian; antimicrobial; and vulnerey; (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
 CC Chagas's cardiomyopathy and coronary arteriosclerosis), angiogenic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to
 CC ABA83193 and AAB50300 represent sequences used in the exemplification of
 CC the present invention.
 XX
 XX Sequence 64 AA;
 SQ
 Query Match 0.6%; Score 8; DB 22; Length 64;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 39 EEEEOKKER 46
 |||||
 DB 29 EEEEOKKER 36
 RESULT 30
 AAB54291
 ID AAB54291 standard; Protein; 95 AA.
 XX
 AC AAB54291;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DB Human pancreatic cancer antigen protein sequence SEQ ID NO:743.
 XX
 KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
 KW detection; diagnosis; identification; cytosolic; neuroprotective;
 KW nootropic; immunomodulatory; relaxant; contraceptive; gynaecological;
 KW antiinflammatory; cardiant; gene therapy; chromosome mapping;
 KW linkage analysis; tissue identification; tissue typing; forensic;
 KW neural; immune system; muscular; reproductive; gastrointestinal;
 KW pulmonary; cardiovascular; renal; proliferative.
 XX
 OS Homo sapiens.
 XX
 PN WO200055320-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05989.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;

XX
 DR MPI; 2000-579444/54.
 DR N-PSDB; AAC99056.
 XX
 XX New nucleic acid that is a pancreatic cancer antigen for preventing,
 PT treating, or ameliorating a medical condition, particular pancreatic
 PT cancer, or for use in assays for diagnosing a pathological condition -
 XX
 XX Claim 11; Page 1188; 1379pp; English.
 XX
 CC AAC98773 to AAC99231 encode the human pancreatic cancer associated
 CC proteins, called pancreatic cancer antigens, given in AAB54008 to
 CC AAB54466. The human pancreatic cancer antigens have cytostatic,
 CC neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
 CC gynaecological, cardiant and antiinflammatory activities, and can be used
 CC in gene therapy. The polynucleotide and proteins can be used for
 CC preventing, treating, or ameliorating a medical condition or in assays
 CC for diagnosing a pathological condition or a susceptibility to one in a
 CC subject. Binding partners to the proteins and the activity of the
 CC proteins can be identified. The pancreatic cancer antigens can be used to
 CC detect, treat or prevent pancreatic disorders, especially cancer.
 CC Agonists and antagonists to the antigens can be screened for. The
 CC pancreatic cancer antigen polynucleotides can be used to design nucleic
 CC acid hybridisation probes that can be used in chromosome mapping, linkage
 CC analysis, tissue identification and/or typing and a variety of forensic
 CC and diagnostic methods. The proteins can be used to generate antibodies
 CC which are used to purify, detect and target the polypeptides, including
 CC both in vivo and in vitro diagnostic and therapeutic methods. The
 CC proteins can be used to treat or prevent neural, immune system, muscular,
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
 CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
 CC sequences used in the exemplification of the present invention.
 XX
 XX Sequence 95 AA;
 SQ
 Query Match 0.6%; Score 8; DB 21; Length 95;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1132 EKLIIQIS 1139
 |||||
 DB 37 EKLIIQIS 44
 RESULT 31
 AAU42144
 ID AAU42144 standard; Protein; 113 AA.
 XX
 AC AAU42144;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DB Propionibacterium acnes immunogenic protein #3040.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 XX
 PR 02-JUN-2000; 2000US-208841P.
 XX
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX

PI Shelly YAM, Persing DH, Mitcham JL, Wang SS, Bhactia A;
PI L'abbondone J, Zhang Y, Jen S, Carter D;
XX WPI; 2001-616774/71.
DR N-PSDB; AAS59516.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
PS Example 1; SEQ ID NO 3339; 1069bp; English.
XX
CC Sequences AAU39105-AAU6017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hyperostosis and osteomyelitis) warts and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 113 AA;

Query Match 0.6%; Score 8; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 908 ESI:SLIRS 915
Db 39 ESI:SLIRS 46

RESULT 32
AAG07152
ID AAG07152 standard; Protein; 152 AA.
XX
AC AAG07152;
XX
AC 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4194.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridization assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123160.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125768.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128214.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129645.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132653.
PR 14-MAY-1999; 99US-0134216.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136392.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138064.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139464.
PR 18-JUN-1999; 99US-0139465.
PR 21-JUN-1999; 99US-0139617.
PR 22-JUN-1999; 99US-0139699.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140891.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142290.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.

PR	19-JUL-1999;	99US-01443332.	PR	13-OCT-1999;	99US-0159294.	PR	13-OCT-1999;	99US-0159294.	PR	13-OCT-1999;	99US-0159294.
PR	19-JUL-1999;	99US-01443333.	PR	13-OCT-1999;	99US-0159295.	PR	13-OCT-1999;	99US-0159295.	PR	13-OCT-1999;	99US-0159295.
PR	19-JUL-1999;	99US-01443334.	PR	14-OCT-1999;	99US-0159320.	PR	14-OCT-1999;	99US-0159320.	PR	14-OCT-1999;	99US-0159320.
PR	19-JUL-1999;	99US-01443335.	PR	14-OCT-1999;	99US-0159330.	PR	14-OCT-1999;	99US-0159330.	PR	14-OCT-1999;	99US-0159330.
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159363.	PR	14-OCT-1999;	99US-0159363.	PR	14-OCT-1999;	99US-0159363.
PR	20-JUL-1999;	99US-0144684.	PR	14-OCT-1999;	99US-0159584.	PR	14-OCT-1999;	99US-0159584.	PR	14-OCT-1999;	99US-0159584.
PR	21-JUL-1999;	99US-0144814.	PR	14-OCT-1999;	99US-0160741.	PR	14-OCT-1999;	99US-0160741.	PR	14-OCT-1999;	99US-0160741.
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160767.	PR	21-OCT-1999;	99US-0160767.	PR	21-OCT-1999;	99US-0160767.
PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160770.	PR	21-OCT-1999;	99US-0160770.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160814.	PR	21-OCT-1999;	99US-0160814.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145192.	PR	21-OCT-1999;	99US-0160815.	PR	21-OCT-1999;	99US-0160815.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.	PR	22-OCT-1999;	99US-0160980.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.	PR	22-OCT-1999;	99US-0160981.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145824.	PR	22-OCT-1999;	99US-0160989.	PR	22-OCT-1999;	99US-0160989.	PR	22-OCT-1999;	99US-0160989.
PR	26-JUL-1999;	99US-0145826.	PR	25-OCT-1999;	99US-0161404.	PR	25-OCT-1999;	99US-0161404.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145813.	PR	25-OCT-1999;	99US-0161405.	PR	25-OCT-1999;	99US-0161405.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145818.	PR	26-OCT-1999;	99US-0161406.	PR	26-OCT-1999;	99US-0161406.	PR	26-OCT-1999;	99US-0161406.
PR	27-JUL-1999;	99US-0145819.	PR	26-OCT-1999;	99US-0161355.	PR	26-OCT-1999;	99US-0161355.	PR	26-OCT-1999;	99US-0161355.
PR	28-JUL-1999;	99US-0145851.	PR	26-OCT-1999;	99US-0161360.	PR	26-OCT-1999;	99US-0161360.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.	PR	26-OCT-1999;	99US-0161361.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161920.	PR	28-OCT-1999;	99US-0161920.	PR	28-OCT-1999;	99US-0161920.
PR	03-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161992.	PR	28-OCT-1999;	99US-0161992.	PR	28-OCT-1999;	99US-0161992.
PR	04-AUG-1999;	99US-0147204.	PR	28-OCT-1999;	99US-0161993.	PR	28-OCT-1999;	99US-0161993.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147202.	PR	29-OCT-1999;	99US-0162142.	PR	29-OCT-1999;	99US-0162142.	PR	29-OCT-1999;	99US-0162142.
PR	05-AUG-1999;	99US-0147192.	PR	Query Match	0.64;	Score 8;	DB 21;	Length 152;	PR	13-OCT-1999;	99US-0159294.
PR	05-AUG-1999;	99US-0147260.	PR	Best Local Similarity	100.06;	Pred. No. 33;			PR	13-OCT-1999;	99US-0159295.
PR	06-AUG-1999;	99US-0147303.	PR	Matches	8;	Conservative	0;	Mismatches	0;	Indels	0;
PR	06-AUG-1999;	99US-0147416.	PR						PR	14-OCT-1999;	99US-0159320.
PR	09-AUG-1999;	99US-0147493.	PR	Oy	1220	DEETSEKF 1227			PR	14-O	

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18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161892.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 0.6%; Score 8; DB 21; Length 152;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 DEPTSEKF 1227
DB 65 DEPTSEKF 72

RESULT 34

ABB61125
ID ABB61125 standard; Protein; 197 AA.

AC ABB61125;

XX 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 10167.

XX Drosophila; developmental biology; cell signalling; insecticide;

XX pharmaceutical.

OS Drosophila melanogaster.

XX W0200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EM;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL05228.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -

XX Disclosure; SEQ ID NO 10167; 21PP + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutic and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA

CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB057737-AB072072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 197 AA;

Query Match 0.6%; Score 8; DB 22; Length 197;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1384 SKYLTILQ 1391
DB 59 SKYLTILQ 66

RESULT 35

AA07151
ID AA07151 standard; Protein; 232 AA.

AC AA07151;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 4193.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132407.

XX 05-MAY-1999; 99US-0132484.

XX 06-MAY-1999; 99US-0132485.

XX 07-MAY-1999; 99US-0132487.

XX 11-MAY-1999; 99US-0132863.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134320.

XX 18-MAY-1999; 99US-0134370.

XX 19-MAY-1999; 99US-0134941.

XX 20-MAY-1999; 99US-0135124.

XX 21-MAY-1999; 99US-0135353.

XX 24-MAY-1999; 99US-0135629.

XX 25-MAY-1999; 99US-0136021.

XX 27-MAY-1999; 99US-0136392.

PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155486.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160988.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161408.
PR 25-OCT-1999; 99US-0161409.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161929.
PR 28-OCT-1999; 99US-0161999.
PR 29-OCT-1999; 99US-0162142.

Query Match 0.6%; Score 8; DB 21; Length 232;
Best Local Similarity 100.0%; Pred. No. 50;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1220 DEETSEXP 1227
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Db 145 DEETSEXP 152
RESULT 37
AAC07150
ID AAC07150 standard; Protein: 239 AA.
XX
AC AAC07150;
XX
DT 17-OCT-2000 (first entry)
DE
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4192.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131448.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
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PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.

AC AAG53553;
XX 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 68193.
DE Protein identification; signal transduction pathway; metabolic pathway;
XX hydrolization assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX EPI033405-A2.
XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-01231825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123180.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126784.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128845.
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PR 21-APR-1999; 99US-0130449.
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PR 28-APR-1999; 99US-0130891.
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PR 30-APR-1999; 99US-0132048.
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PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139859.
PR 23-JUN-1999; 99US-0140353.
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PR 24-JUN-1999; 99US-0140685.
PR 28-JUN-1999; 99US-0140823.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
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PR 21-JUL-1999; 99US-0144814.
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PR 21-JUL-1999; 99US-0145086.
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PR 23-JUL-1999; 99US-0145145.
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PR 27-JUL-1999; 99US-0145513.
PR 27-JUL-1999; 99US-0145518.
PR 28-JUL-1999; 99US-0145519.
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PR 02-AUG-1999; 99US-0146386.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
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PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149829.
PR 23-AUG-1999; 99US-0149802.
PR 23-AUG-1999; 99US-0149930.
PR 23-AUG-1999; 99US-0150566.

PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
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 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
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 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
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 PR 12-OCT-1999; 99US-0158369.
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 PR 13-OCT-1999; 99US-0159294.
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 PR 18-OCT-1999; 99US-0159584.
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 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
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 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 0.6%; Score 8; DB 21; Length 239;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1220 DEBTSKRF 1227
 DB 152 DEBTSKRF 159

RESULT 39
 AAB53281
 ID AAB53281 standard; Protein; 259 AA.

AC AAB53281;
 XX 09-MAR-2001 (first entry)
 DT Human colon cancer antigen protein sequence SEQ ID NO:821.
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW

KW identification; cyrostatic; cardiactive; neuroprotective; vulnary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antineflective; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.

OS Homo sapiens.
 EN W0200055351-A1.

PD 21-SEP-2000.

XX 08-MAR-2000; 2000MO-US05883.

XX 12-MAR-1999; 99US-0124270.

PA (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI: 2000-587534/55.

DR N-PSDB; AAC98038.

PT Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer -

XX Claim 11; Page 1374; 2104pp; English.

XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cyrostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal;
 CC vulnary, nephrotropic, antineflective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins
 CC may also be used to prevent diseases such as neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, wounds, renal disorders, infectious
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
 CC AAC54007 represent sequences used in the exemplification of the present
 CC invention.

SO Sequence 259 AA;

Query Match 0.6%; Score 8; DB 21; Length 259;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 EEBROKRF 46
 DB 174 EEBROKRF 181

RESULT 40
 AAG07235
 ID AAG07235 standard; Protein; 358 AA.

AC AAG07235;
 XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 4311.

KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 OS Arabidopsis thaliana.

XX EP1033405-A2.
PR 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0122180.
PR 05-MAR-1999; 99US-0122348.
PR 23-MAR-1999; 99US-0125788.
PR 23-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131049.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
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PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0133486.
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PR 07-MAY-1999; 99US-0133863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 20-MAY-1999; 99US-0135124.
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PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 01-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137520.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138029.
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PR 10-JUN-1999; 99US-0138844.
PR 14-JUN-1999; 99US-0139119.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
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PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158359.
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PR 13-OCT-1999; 99US-0159295.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161933.
PR 29-OCT-1999; 99US-0162142.

Query Match 0.6%; Score 8; DB 21; Length 358;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 145 LKSLRRCG 152
DB 80 LKSLRRCG 87

RESULT 41

AAAG48600
ID AAC48600 standard; Protein; 358 AA.

AC AAG48600;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 61391.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hydriasiation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX EPI033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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 DB 80 LKSRKGC 87

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 AC ABB92886;
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 DT 31-MAY-2002 (first entry)
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 XX
 KW Herbicidal; plant; agriculture; herbicide.
 XX
 OS Arabidopsis thaliana.
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 PN MO200210210-A2.
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 PD 07-FEB-2002.
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 PF 28-AUG-2001; 2001MO-EP09892.
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 PR 28-AUG-2001; 2001MO-EP09892.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Tietjen K, Weidner M,
 XX
 DR WP; 2002-269010/31.
 XX
 PT Identifying plant target proteins for herbicidally active compounds,

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PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms -
PS Claim 5; SEQ ID NO 2097; 261pp + Sequence Listing; English.
XX
XX The invention relates to identifying target proteins
CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
CC aligning and comparing nucleic acid or amino acid sequences from plant
CC with nucleic acid or amino acid sequences from non-plant organisms using
CC suitable search parameters, where plant sequences having an E-value
CC greater by a factor of 3 than the E-value of most similar non-plant
CC sequences are selected. The polypeptides or nucleic acids encoding them
CC are useful for identifying modulators. The identified modulators are
CC useful as herbicides.
SQ
SQ Sequence 358 AA;
QY
QY 145 LKSRIRGG 152
QY |||||
DB 80 LKSRIRGG 87
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AC AAG48599;
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XX 18-OCT-2000 (first entry)
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DT Arabidopsis thaliana protein fragment SEQ ID NO: 61390.
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XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
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XX Arabidopsis thaliana.
OS
OS Ep1033405-A2.
XX
XX 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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Best Local Similarity 100.04; Pred. No. 79;
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Db 145 LKSRRCG 152
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RESULT 44
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ID AACG7234 standard; Protein; 374 AA.
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AC AACG7234;
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XX 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 4310.
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 4310.
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KW Protein identification: signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0152163.
PR 07-SEP-1999; 99US-0152163.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161320.

PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 0.6%; Score 8; DB 21; Length 374;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 LKSRURGG 152
DB 96 LKSRURGG 103

RESULT 45
AAR12352

ID AAR12352 standard; Protein; 428 AA.

XX AAR12352;

XX 14-AUG-1991 (first entry)

XX Toxoplasma gondii P66 antigen.

XX Toxoplasma gondii; vaccine; P66.

XX Toxoplasma gondii.

XX EP431541-A.

XX 12-JUN-1991.

XX 04-DEC-1990; 90EP-0123152.

XX 08-DEC-1989; 89DE-3940598.

XX (BEHW) BEHRINGWERKE AG.

XX Knapp S, Zieglmaier R, Kupper H;

XX WPI; 1991-172854/24.

XX N-PSDB; AAQ11918.

XX New Toxoplasma gondii protein, nucleic acid and derived
PT antibodies - useful as diagnostic reagents, vaccines and for
PT treatment

XX Claim 1; Table 10; 28pp; German.

XX A cDNA fragment encoding P66 was isolated from a T.gondii gene
CC bank. Recombinant protein was produced as part of a fusion protein
CC with beta-galactosidase. The hybrid protein was found to react
CC specifically with IgG antibodies in most of the 21 serum samples
CC tested from humans with acute and chronic T.gondii infection.
CC c.f. P66 and P35 hybrid proteins (see AAR12351 and AAR12353) which
CC reacted with all 21 samples.
CC See also AAQ11909-Q11917 and AAQ11919.

XX Sequence 428 AA;

Query Match 0.6%; Score 8; DB 12; Length 428;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FGAGLTRL 112
DB 395 FGAGLTRL 402

RESULT 46
AAV34752

ID AAV34752 standard; Protein; 441 AA.

XX AAV34752;

XX 13-SEP-1999 (first entry)

XX Chlamydia pneumoniae transmembrane protein sequence.

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis;

XX vaccine; neutralising epitope.

XX Chlamydia pneumoniae.

XX WO9927105-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98NO-1B01890.

XX 04-NOV-1998; 98US-0107078.

XX 21-NOV-1997; 97FR-0014673.

XX (GSEST) GENSET.

XX Griffats R;

XX WPI; 1999-357842/30.

XX Genome sequence of Chlamydia pneumoniae

XX Page 739-740; Disclosure; 1912pp; English.

XX AAV34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAV31990) of Chlamydia pneumoniae.
CC C. pneumoniae causes respiratory disease such as pneumonia and
CC bronchitis and is thought to be a contributing factor in heart
CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAV34584-Y35879) can be used in
CC nucleotide sequences as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae.

XX Sequence 441 AA;

Query Match 0.6%; Score 8; DB 20; Length 441;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 LILFGAGL 109
DB 135 LILFGAGL 142

RESULT 47
AAW19745

ID AAW19745 standard; Protein; 496 AA.

XX AAW19745;

XX 16-SEP-1997 (first entry)

XX Mouse inhibitor of apoptosis protein homologue MHA.

XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MHA;

XX degenerative disease; infectious disease; autoimmune disease;

XX cancer; therapy; diagnosis.

XX Mus musculus.

XX Key Location/Qualifiers
XX Region 26..93
XX Region /label= BIR
XX Region 163..230


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FT      /label= BIR
FT      Region      264..330
FT      /label= BIR
FT      Region      448..485
FT      /label= RING_finger
XX      MO9723501-A1.
XX      03-JUL-1997.
XX      PD
XX      20-DEC-1996; 96WO-AU00827.
XX      PF
XX      22-DEC-1995; 95AU-0007275.
XX      PR
XX      (AMBA-) AMRAD OPERATIONS PTY LTD.
XX      PA
XX      Vaux DL;
XX      PI
XX      WPI; 1997-350966/32.
XX      DR
XX      N-PSDB; AAT72710.
XX      PT
XX      Isolated protein homologues of viral inhibitors of apoptosis - used
XX      to modulate apoptosis for treatment of degenerative, infectious or
XX      autoimmune diseases and cancer
XX      PS
XX      Claim 7; Page 44-47; 136pp; English.
XX      CC
XX      Mammalian IAP homologue A (MIMA) (AAW19745) is a murine homologue of
XX      baculovirus inhibitor of apoptosis protein (IAP). Its amino acid
XX      sequence was deduced from a cDNA clone (see also AAT72710) isolated
XX      from a mouse liver cDNA library on the basis of homology to Oxygia
XX      pseudotsugata polyhedrosis virus IAP BIR and RING finger amino acid
XX      motifs (see also AAW19744). IAP homologues (see also AAW19746-52) and
XX      their derivatives and chemical analogues can be used in methods for
XX      modulating apoptosis in animal cells, specifically for treatment,
XX      by inhibition, of degenerative and infectious disease or, by
XX      promotion, of cancer and autoimmune disease.
XX      SQ
XX      Sequence 496 AA;

Query Match      0.6%; Score 8; DB 18; Length 496;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      193 DTVOCFSC 200
DB      59 DTVOCFSC 66

```

RESULT 48

```

AAW19584
ID      AAW19584 standard; Protein; 496 AA.
XX
AC      AAW19584;
XX
DT      02-SEP-1997 (first entry)
XX
DE      Mouse apoptosis inhibitor M-XIAP.
XX
KM      Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
KM      M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;
KM      ischaemia; myocardial infarction; stroke;
KM      reperfusion injury; toxin-induced liver disease; gene therapy;
XX      diagnosis.
XX
OS      Mus sp.
XX
FH      Key
FH      Location/Qualifiers
FT      26..93
FT      /label= BIR-1
FT      163..230
FT      /label= BIR-2
FT      264..329
FT      Domain

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```

FT      /label= BIR-3
FT      Domain      438..483
FT      /label= RING_zinc_finger
XX      MO9706255-A2.
XX      20-FEB-1997.
XX      PD
XX      05-AUG-1996; 96WO-IB01022.
XX      PF
XX      22-DEC-1995; 95US-0576956.
XX      PR
XX      04-AUG-1995; 95US-0511485.
XX      PA
XX      (UYOT-) UNIV OTTAWA.
XX      PI
XX      Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX      WPI; 1997-154262/14.
XX      DR
XX      N-PSDB; AAT70839.
XX      PT
XX      Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
XX      to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
XX      of susceptibility to apoptotic disease
XX      PS
XX      Claim 27; Page 79-80; 213pp; English.
XX      CC
XX      Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
XX      M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
XX      are inhibitors of apoptosis (IAP) and which are characterised by
XX      the presence of a ring zinc finger domain (see also AAW19587) and at
XX      least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
XX      The M-XIAP amino acid sequence was deduced from the m-xiap gene
XX      (AAT70839) isolated from a mouse embryo cDNA library. The IAP
XX      polypeptides can be expressed in host cells (in vitro or in
XX      vivo) and used in methods for treating diseases and disorders
XX      involving apoptosis, esp. in a human diagnosed as HIV-positive or
XX      as having AIDS, a neurodegenerative disease, a myelodysplastic
XX      syndrome or an ischaemic injury, selected from myocardial infarction,
XX      stroke, reperfusion injury, or a toxin-induced liver disease.
XX      SQ
XX      Sequence 496 AA;

Query Match      0.6%; Score 8; DB 18; Length 496;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      193 DTVOCFSC 200
DB      59 DTVOCFSC 66

```

RESULT 49

```

AAW63297
ID      AAW63297 standard; Protein; 496 AA.
XX
AC      AAW63297;
XX
DT      13-NOV-1998 (first entry)
XX
DE      Murine XIAP protein.
XX
KM      Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KM      proliferative disease; IAP; therapy; cancer; mouse; XIAP protein.
XX
OS      Mus sp.
XX
PN      WO9835693-A2.
XX      20-AUG-1998.
XX      PD
XX      13-FEB-1998; 98WO-IB00781.
XX      13-FEB-1997; 97US-0800929.
XX      PR

```

XX (UYOT-) UNIV OTTAWA.
 PA
 XX
 XX Baird S, Korneluk R, Liston P, Mackenzie AR, Pratt C;
 PI Teang B;
 XX
 DR WPI; 1998-467164/40.
 XX N-PSDB; AAV55041.
 XX
 PT Inducing apoptosis in proliferative mammalian cells with inhibitor
 PT of IAP or NAIP polypeptide - also methods for prognosis based on
 PT presence of IAP and NAIP, specifically applied to cancers involving
 PT p53 mutations
 XX
 PS Disclosure; Fig 4; 147pp; English.
 XX
 CC This sequence is the murine XIAP protein, which is a inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,
 CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors.
 XX
 SQ Sequence 496 AA;
 Query Match 0.6%; Score 8; DB 19; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 193 DTVOCFSC 200
 Db 59 DTVOCFSC 66
 RESULT 50
 ABG5666
 ID ABG5666 standard; Protein; 496 AA.
 AC
 XX ABG5666;
 AC
 XX
 DT 26-AUG-2002 (first entry)
 DE
 XX Mouse inhibitor of apoptosis, XIAP.
 XX
 KW Mouse; antisense; inhibitor of apoptosis; H1AP1, H1AP2; XIAP;
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Mus sp.
 XX
 PN WO200226968-A2.
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-CA01379.
 XX
 PR 28-SEP-2000; 2000US-0672717.
 XX
 PA (UYOT-) UNIV OTTAWA
 PA (ABGE-) ABGEA THERAPEUTICS INC.
 XX

PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX
 XX WPI/ 2002-479562/51.
 DR N-PSDB; ABK93872.
 XX
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for
 PT enhancing apoptosis in a cell, for treating cancer and other
 PT proliferative diseases
 XX
 PS Example 12; Fig 4; 135pp; English.
 XX
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, H1AP1 or H1AP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
 CC protein sequence.
 XX
 SQ Sequence 496 AA;
 Query Match 0.6%; Score 8; DB 23; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 193 DTVOCFSC 200
 Db 59 DTVOCFSC 66
 RESULT 51
 ABP72157
 ID ABP72157 standard; Protein; 496 AA.
 AC
 XX ABP72157;
 AC
 XX
 DT 22-APR-2003 (first entry)
 DE
 XX Mouse inhibitor of apoptosis protein MIAP3.
 XX
 KW Inhibitor of apoptosis; MIAP3; mouse; apoptosis; cancer; leukemia;
 KW lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic;
 KW gene therapy.
 XX
 OS Mus sp.
 XX
 PN WO2003004606-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 03-JUL-2002; 2002WO-US21002.
 XX
 PR 03-JUL-2001; 2001US-0898158.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Troy CM, Shelanski ML;
 XX
 DR WPI; 2003-210351/20.
 DR N-PSDB; ABZ58102.
 XX
 PT New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for

PT treating cancer, neurodegenerative disorder or cardiomyopathy -

XX

PS Disclosure; Fig 15A, 124pp; English.

XX

CC The present sequence is the protein sequence of murine inhibitor of

CC apoptosis protein MIAP3. The invention provides a nucleic acid,

CC such as an antisense oligonucleotide, which specifically hybridises

CC to a nucleic acid encoding an inhibitor of apoptosis protein,

CC especially MIAP1, MIAP2, MIAP3, CIAP1, CIAP2 and XIAP. A claimed

CC method for inducing a cell's death comprises contacting the cell

CC with the nucleic acid under conditions permitting the nucleic acid

CC to enter the cell, especially the use of a vector, liposome, or a

CC mechanical or electrical means. The method is used to treat acute

CC lymphocytic leukaemia, acute myelogenous leukaemia, lung cancer,

CC breast cancer, ovarian cancer, prostate cancer, lymphoma, Hodgkin's

CC disease, malignant melanoma, neuroblastoma, renal cell carcinoma

CC and squamous cell carcinoma (all claimed).

CC

SQ Sequence 496 AA;

Query Match 0.6%; Score 8; DB 24; Length 496;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTNOCFSC 200

Db 59 DTNOCFSC 66

RESULT 52

ID ABP41530 standard; Protein; 506 AA.

XX

AC ABP41530;

XX

DT 22-AUG-2002 (first entry)

XX

DE Human ovarian antigen HF1A44, SEQ ID NO:2662.

XX

KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;

KW ovarian cancer; breast cancer; tumour; reproductive system disorder;

KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;

KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;

KW inflammatory condition; immune disorder; blood disorder;

KW cardiovascular disorder; respiratory disorder; neurological disorder;

KW gastrointestinal disorder; urinary system disorder; drug screening;

KW gene therapy; chromosome mapping; forensic analysis;

KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;

KW antiinflammatory; gynaecological; reproductive; chromosome 14.

XX

OS Homo sapiens.

XX

PN WO200200677-A1.

XX

PD 03-JAN-2002.

XX

PF 07-JUN-2001; 2001WO-US18569.

XX

PR 07-JUN-2000; 2000US-209467P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Birse CE, Rosen CA;

XX

DR WPI: 2002-147878/19.

XX

DR N-Psdb; ABQ54607.

XX

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,

PT useful in the prevention, treatment and diagnosis of cancer (e.g.

PT ovarian cancer), immune disorders, cardiovascular disorders and

PT neurological diseases -

PS Claim 11, SEQ ID No 2662; 2922pp; English.

XX

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-

CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also

CC encompasses polypeptides 90% identical and polynucleotides 95% identical

CC to the sequences of the invention. The invention additionally relates to

CC recombinant vectors and host cells comprising human ovarian antigen

CC polynucleotides, antibodies against human ovarian antigens, and the use

CC of ovarian antigen polynucleotides and polypeptides in diagnosing,

CC treating, prophosing or preventing various ovary and/or breast-related

CC disorders. Such conditions include ovarian cancer and breast cancer, and

CC metastatic tumours of ovarian or breast origin, reproductive system

CC disorders (e.g., infertility, disorders of pregnancy, anovulation,

CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine

CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic

CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and

CC vaginitis), immune disorders (e.g., congenital and acquired

CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),

CC blood-related disorders (e.g., anaemia), cardiovascular disorders,

CC respiratory disorders, neurological disorders, gastrointestinal disorders

CC and urinary system disorders. Ovarian antigen polypeptides and

CC polynucleotides may also be used in screening for compounds which

CC modulate ovarian antigen expression or activity. The polynucleotides may

CC further be used for gene therapy, chromosome mapping, in the

CC identification of individuals and in forensic analysis, and the

CC polypeptides may be used as food additives or to prepare antibodies

CC useful in disease diagnosis, drug targeting and phenotyping. The present

CC sequence represents a human ovarian antigen of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

CC

SQ Sequence 506 AA;

Query Match 0.6%; Score 8; DB 23; Length 506;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 EEEBOKER 46

Db 483 EEEBOKER 490

RESULT 53

ABG09940

ID ABG09940 standard; Protein; 519 AA.

XX

AC ABG09940;

XX

DT 13-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #9931.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US08631.

XX

PR 31-MAR-2000; 2000US-0540217.

XX

PR 23-AUG-2000; 2000US-0649167.

XX

PA (HUSE-) HXSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI: 2001-639362/73.

XX

DR N-Psdb; AAS74127.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

PS Claim 20; SEQ ID NO 40299; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridization probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG0377 represent novel human
CC diagnostic amino acid sequences of the invention
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 519 AA;

Query Match 0.6%; Score 8; DB 22; Length 519;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 EEEBOKER 46
|||||
434 EREBOKER 441

Db 434 EREBOKER 441

RESULT 54
ABBB1920
ID ABBB1920 standard; Protein; 521 AA.
XX
XX ABBB1920;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 12552.
DE
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KM pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PR
XX
XX 11-JUL-2000; 2000US-0614150.
PT
XX
XX (PEKE) PE CORP NY.
PA
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX
XX WPI; 2001-656860/75.
DR
XX
XX N-PSDB; AB106023.
XX
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell

PT interactions -

XX

PS Disclosure; SEQ ID NO 12552; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB101840-AB116175) and the encoded DNA
CC sequences (AB101840-AB116175) and the encoded proteins
CC (AB101840-AB116175).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 521 AA;

Query Match 0.6%; Score 8; DB 22; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 GLDAVOIA 35
|||||
233 GLDAVOIA 240

Db 233 GLDAVOIA 240

RESULT 55
AAR71976
ID AAR71976 standard; Protein; 523 AA.
XX
XX AAR71976;
AC
XX
XX 25-MAR-2003 (updated)
DT
XX
XX 15-MAR-1995 (first entry)
DT
XX
XX Pertussis A.
DE
XX
XX Bordetella pertussis ptx operon; holotoxin; pertussis A and B.
KM
XX
XX Bordetella pertussis.
OS
XX
XX EP618294-A1.
PN
XX
XX 05-OCT-1994.
PD
XX
XX 15-MAR-1994; 94EP-0104006.
PF
XX
XX 15-MAR-1993; 93US-0031619.
PR
XX
XX (AMCY) AMERICAN CYANAMID CO.
PA
XX
XX Baker SM, Deich RA;
PI
XX
XX WPI; 1994-304463/38.
DR
XX
XX N-PSDB; AAQ74445.
PT
XX
XX Cloned region of Bordetella pertussis genome encoding holo:toxin
PT - is located 3' of the ptx operon, and is used for expression and
PT secretion of holo:toxin for vaccine use

PS Example 1; Fig 1; 26pp; English.

XX AAQ74445 is a DNA sequence located 3' of the Bordetella pertussis (BP)
CC ptx operon. It encodes pertussis A (AAR71976) and B (AAR72100); these
CC gene products are involved in the expression or secretion of BP
CC holotoxin. AAQ74445 was used in the construction of a plasmid, which
CC enabled the expression, assembly and secretion of BP holotoxin, which
CC regulated in a homologous or heterologous host. These hosts could then be
CC used for the production of large quantities of holotoxin, for use as a
CC vaccine.
CC (updated on 25-MAR-2003 to correct PN field.)
XX

```

SQ Sequence 523 AA;
Query Match 0.6%; Score 8; DB 15; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 473 GSGKTVLL 480
    |||||
DB 459 GSGKTVLL 466

RESULT 56
ABB67078
ID ABB67078 standard; Protein; 538 AA.
AC
XX
XX ABB67078;
XX
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 28026.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001MO-US09231.
XX
XX 23-MAR-2000; 2000OUS-191637P.
XX 11-JUL-2000; 2000OUS-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX MPI; 2001-656860/75.
XX
XX N-PSDB; ABL11181.
XX
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Disclosure; SEQ ID NO 28026; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABR57737-ABR72072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
XX Sequence 538 AA;

Query Match 0.6%; Score 8; DB 22; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 292 SAVGVALL 299
    |||||
DB 340 SAVGVALL 347

RESULT 57
AAW80788
AAW80788
ID AAW80788 standard; Protein; 567 AA.
AC
XX
XX AAW80788;
XX
XX 01-MAR-1999 (first entry)
XX
XX Polypeptide fragment encoded by gene 36.
XX
XX
XX DE Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal;
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
XX
XX OS Homo sapiens.
XX
XX
XX PN WO9854963-A2.
XX
XX
XX PD 10-DEC-1998.
XX
XX
XX PF 04-JUN-1998; 98MO-US11422.
XX
XX
XX PR 18-DEC-1997; 97US-0070923.
XX PR 06-JUN-1997; 97US-0048877.
XX PR 06-JUN-1997; 97US-0048881.
XX PR 06-JUN-1997; 97US-0048884.
XX PR 06-JUN-1997; 97US-0048893.
XX PR 06-JUN-1997; 97US-0048896.
XX PR 06-JUN-1997; 97US-0048899.
XX PR 06-JUN-1997; 97US-0048915.
XX PR 06-JUN-1997; 97US-0048949.
XX PR 06-JUN-1997; 97US-0048964.
XX PR 06-JUN-1997; 97US-0048972.
XX PR 06-JUN-1997; 97US-0049020.
XX PR 06-JUN-1997; 97US-0049375.
XX PR 05-SEP-1997; 97US-0057628.
XX PR 05-SEP-1997; 97US-0057635.
XX PR 05-SEP-1997; 97US-0057644.
XX PR 05-SEP-1997; 97US-0057647.
XX PR 05-SEP-1997; 97US-0057650.
XX PR 05-SEP-1997; 97US-0057661.
XX PR 05-SEP-1997; 97US-0057667.
XX PR 05-SEP-1997; 97US-0057761.
XX PR 05-SEP-1997; 97US-0057764.
XX PR 05-SEP-1997; 97US-0057770.
XX PR 05-SEP-1997; 97US-0057775.
XX PR 05-SEP-1997; 97US-0057778.
XX PR 06-JUN-1997; 97US-0048875.
XX PR 06-JUN-1997; 97US-0048878.
XX PR 06-JUN-1997; 97US-0048882.
XX PR 06-JUN-1997; 97US-0048885.
XX PR 06-JUN-1997; 97US-0048894.
XX PR 06-JUN-1997; 97US-0048897.
XX PR 06-JUN-1997; 97US-0048900.
XX PR 06-JUN-1997; 97US-0048916.
XX PR 06-JUN-1997; 97US-0048962.
XX PR 06-JUN-1997; 97US-0048970.
XX PR 06-JUN-1997; 97US-0048974.
XX PR 06-JUN-1997; 97US-0049373.
XX PR 05-SEP-1997; 97US-0057584.
XX PR 05-SEP-1997; 97US-0057629.
XX PR 05-SEP-1997; 97US-0057642.
XX PR 05-SEP-1997; 97US-0057645.
XX PR 05-SEP-1997; 97US-0057648.
XX PR 05-SEP-1997; 97US-0057651.
XX PR 05-SEP-1997; 97US-0057662.
XX PR 05-SEP-1997; 97US-0057668.
XX PR 05-SEP-1997; 97US-0057762.
XX PR 05-SEP-1997; 97US-0057765.
XX PR 05-SEP-1997; 97US-0057771.
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PR 05-SEP-1997; 97US-0057776.
 PR 06-JUN-1997; 97US-0048876.
 PR 06-JUN-1997; 97US-0048880.
 PR 06-JUN-1997; 97US-0048883.
 PR 06-JUN-1997; 97US-0048892.
 PR 06-JUN-1997; 97US-0048895.
 PR 06-JUN-1997; 97US-0048898.
 PR 06-JUN-1997; 97US-0048901.
 PR 06-JUN-1997; 97US-0048917.
 PR 06-JUN-1997; 97US-0048963.
 PR 06-JUN-1997; 97US-0048971.
 PR 06-JUN-1997; 97US-0049019.
 PR 05-SEP-1997; 97US-0049374.
 PR 05-SEP-1997; 97US-0057627.
 PR 05-SEP-1997; 97US-0057634.
 PR 05-SEP-1997; 97US-0057643.
 PR 05-SEP-1997; 97US-0057649.
 PR 05-SEP-1997; 97US-0057654.
 PR 05-SEP-1997; 97US-0057666.
 PR 05-SEP-1997; 97US-0057760.
 PR 05-SEP-1997; 97US-0057763.
 PR 05-SEP-1997; 97US-0057769.
 PR 05-SEP-1997; 97US-0057774.
 PR 05-SEP-1997; 97US-0057777.
 XX (HUMA-) HUMAN GENOME SCI INC.

PI Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA,
 PI Fan P, Ferrie AM, Fischer CL, Florence C,
 PI Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW,
 PI Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM,
 PI Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
 DR WPI; 1999-059865/05.
 DR N-PSDB; AAV84446.

XX New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Disclosure; Page 30; 772pp; English.

XX The invention relates to nucleic acid sequences (AAV84411 to AAV84633)
 CC encoding human secreted proteins (AAV84534 to AAV84756). The secreted
 CC protein gene sequences are deposited with the ATCC under deposit numbers
 CC ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
 CC 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
 CC cells comprising recombinant vectors containing the nucleic acid
 CC sequences are used for the recombinant production of the secreted
 CC protein. The polynucleotide and amino acid sequences are useful for
 CC useful for preventing, treating or ameliorating medical conditions e.g.
 CC by protein or gene therapy. Pathological conditions can be also
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the polynucleotides, based on
 CC which tissues they are most highly expressed in, and include developing
 CC products for the diagnosis or treatment of cancer, neurodegenerative
 CC disorders, developmental abnormalities and foetal deficiencies, blood
 CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
 CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
 CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
 CC osteoporosis, prostate diseases, obesity, disorders involving osteoclasts
 CC such as osteoporosis, arthritis or malignancies, diseases of testes,
 CC lung or thymus, digestive/endocrine disorders, infections and AIDS. The
 CC polypeptides are also useful for identifying their binding partners.
 CC The present sequence represents a polypeptide fragment encoded by a
 CC gene of the invention (see descriptor line for gene number).

XX Sequence 567 AA;
 Query Match 0.6%; Score 8; DB 20; Length 567;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 39 EREBECKER 46
 Db 483 EREBECKER 490

RESULT 58
 ABB50625
 ID ABB50625 standard; Protein; 567 AA.
 AC ABB50625;
 XX
 DT 07-FEB-2002 (first entry)

Human secreted protein encoded by gene 36 SEQ ID NO:573.

XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
 KW dermatological; immunosuppressive; anti-inflammation; immunostimulant;
 KW cytoskeletal; cardiac; vascular; anti-angiogenic; ophthalmological;
 KW neuroprotective; nootropic; anticonvulsant; antialzheimer; vulnary;
 KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
 KW Gaucher's disease; cardiovascular disease; Schmitz syndrome; chemotaxis;
 KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiotensin disorder;
 KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;
 KW Parkinson's disease; infectious disease; chromosome 14.

Homoe sapiens.

PN WO200162891-A2.

XX 30-AUG-2001.

XX 21-FEB-2001; 2001WO-US05614.

XX 24-FEB-2000; 2000US-184836P.

XX 29-MAR-2000; 2000US-193170P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA,
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y,
 PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P,
 PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G,
 PI Zeng Z, Greene JM;
 DR WPI; 2001-625724/72.

XX Nucleic acids encoding 207 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -

XX Disclosure; Page 84-85; 1533pp; English.

XX ABB50301 to ABB51287 and ABB83194 to ABB83441 represent human secreted
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 CC activities based on the tissues and cells the genes are expressed in.
 CC Example of these activities include: immunomodulatory; antisclerotic;
 CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 CC anti-HIV; cytoskeletal; cardiac; anti-angiogenic; ophthalmological;
 CC neuroprotective; nootropic; anticonvulsant; antialzheimer; vascular;
 CC antiparkinsonian; antimicrobial; and vulnary. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. Schmitz syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,

CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis; ABA83185 to
 CC ABA83193 and ABA850300 represent sequences used in the exemplification of
 CC the present invention.

XX SQ Sequence 567 AA;

Query Match 0.6%; Score 8; DB 22; Length 567;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 EEEEXKER 46
 |||||
 DB 483 EEEEXKER 490

RESULT 59

AA85658
 ID AAY85658 standard; Protein; 568 AA.

XX AAY85658;

DT 12-FEB-2001 (first entry)

XX Human Acinus S protein sequence.

XX Chromatin aggregation induction; human; Acinus; AIDS; herpes; diabetes;
 KW Alzheimer's disease; Parkinson's disease; cardiac infection;
 KW brain infection; adenovirus infection; viral hepatitis.

XX Homo sapiens.

XX WO200061743-A1.

XX 19-OCT-2000.

XX 07-APR-2000; 2000WO-JP02254.

XX 09-APR-1999; 99JP-0103317.

XX (SHIO) SHIONOGI & CO LTD.

XX Sahara S, Eguchi Y, Tsujimoto Y;

XX WPI; 2000-665130/64.

XX N-PSDB; AAC61197.

XX A novel polypeptide which induces chromatin aggregation but is not
 PT involved in DNA fragmentation used for the regulation of apoptosis and
 PT screening of potential apoptosis inhibitors

XX Disclosure; Page 91-95; 99JP; Japanese.

XX This invention relates to a polypeptide which induces chromatin
 CC aggregation. The polypeptide is a fragment of the human Acinus protein.
 CC Included in the invention is a nucleotide sequence encoding the
 CC polypeptide, antisense oligonucleotides, antibodies recognizing the
 CC polypeptide sequence, and apoptosis regulating agents containing the
 CC oligonucleotides. Also included in the invention is a method for
 CC screening compounds for their activity as chromatin aggregation
 CC inhibitors, regulators or promoters. The polypeptide induces chromatin
 CC aggregation within the cell nucleus without inducing DNA fragmentation.
 CC The polypeptide can be used in the investigation and treatment of
 CC diseases in which apoptosis is implicated, including AIDS, Alzheimer's
 CC disease, Parkinson's disease, cardiac or brain infection, herpes or
 CC adenovirus infection, diabetes and viral hepatitis. The present sequence
 CC represents the human Acinus protein.

XX SQ Sequence 568 AA;

Query Match 0.6%; Score 8; DB 21; Length 568;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 39 EEEEXKER 46
 |||||
 DB 483 EEEEXKER 490

RESULT 60

ABA871239
 ID ABA871239 standard; Protein; 575 AA.

XX ABA871239;

DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 40509.

XX Drosophila; developmental biology; cell signalling; insecticide;
 KW Pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PERE) PE CORP NY.

XX Venter JC, Adams M, Li PMD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL15342.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions

XX Disclosure; SEQ ID NO 40509; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (AB5737-AB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 575 AA;

Query Match 0.6%; Score 8; DB 22; Length 575;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 292 SAVGVAML 299
 |||||
 DB 377 SAVGVAML 384

RESULT 61

AA85659
 ID AAY85659 standard; Protein; 583 AA.

XX AAY85659;

DT 12-FEB-2001 (first entry)
 XX Human Actinase S' protein sequence.
 XX Chromatin aggregation induction; human; Actinase; AIDS; herpes; diabetes;
 KM Alzheimer's disease; Parkinson's disease; cardiac infection;
 KM brain infection; adenovirus infection; viral hepatitis.
 XX Homo sapiens.
 XX WO200061743-A1.
 XX 19-OCT-2000.
 XX 07-APR-2000; 2000WO-JP02254.
 XX 09-APR-1999; 99JP-0103317.
 XX (SHIO) SHIONOGI & CO LTD.
 XX Sahara S, Eguchi Y, Tsujimoto Y;
 PI MPI; 2000-665130/64.
 DR N-PSDB; AAC61198.
 XX A novel polypeptide which induces chromatin aggregation but is not
 PT involved in DNA fragmentation used for the regulation of apoptosis and
 PT screening of potential apoptosis inhibitors -
 PS Disclosure; Page 67-70; 99pp; Japanese.
 XX This invention relates to a polypeptide which induces chromatin
 CC aggregation. The polypeptide is a fragment of the human Actinase protein.
 CC included in the invention is a nucleotide sequence encoding the
 CC polypeptide, antisense oligonucleotides, antibodies recognizing the
 CC polypeptide sequence, and apoptosis regulating agents containing the
 CC oligonucleotides. Also included in the invention is a method for
 CC screening compounds for their activity as chromatin aggregation
 CC inhibitors, regulators or promoters. The polypeptide induces chromatin
 CC aggregation within the cell nucleus without inducing DNA fragmentation.
 CC The polypeptide can be used in the investigation and treatment of
 CC diseases in which apoptosis is implicated, including AIDS, Alzheimer's
 CC disease, Parkinson's disease, cardiac or brain infection, herpes or
 CC adenovirus infection, diabetes and viral hepatitis. The present sequence
 CC represents the human Actinase protein.
 XX
 XX Sequence 583 AA;
 SQ
 Query Match 0.6%; Score 8; DB 21; Length 583;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 39 EEEOKER 46
 DB 498 EEEOKER 505
 RESULT 62
 AAG09939
 ID AAG09939 standard; Protein; 614 AA.
 XX
 XX AAG09939;
 AC
 XX 13-FEB-2002 (first entry)
 DT
 XX Novel human diagnostic protein #9930.
 DE
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 XX Homo sapiens.
 OS
 XX

PN WO200175067-A2.
 XX
 XX 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US08611.
 PF
 XX 31-MAR-2000; 2000US-0540217.
 XX 23-AUG-2000; 2000US-0649167.
 XX (HYSB-) HYSBQ INC.
 XX
 XX Drmanac RT, Liu C, Tang YT;
 PI MPI; 2001-639362/73.
 DR N-PSDB; AAG74126.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PT
 PS Claim 20; SEQ ID NO 40298; 103pp; English.
 XX
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridization probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAG00010-AAG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 614 AA;
 SQ
 Query Match 0.6%; Score 8; DB 22; Length 614;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 39 EEEOKER 46
 DB 529 EEEOKER 536
 RESULT 63
 AAY57754
 ID AAY57754 standard; Protein; 654 AA.
 XX
 XX AAY57754;
 AC
 XX 16-MAR-2000 (first entry)
 DT
 XX CKS-P66-CKS fusion protein protein sequence.
 DE
 XX Toxoplasmosis; antigen; P29; vaccine; coccidiostatic; antibody;
 KM diagnosis; infection; identification.
 XX
 XX Toxoplasma gondii.
 OS
 XX Synthetic.
 XX
 XX Key Location/Qualifiers


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FT Misc-difference 251 /note= "unspecified"
XX
XX
XX WO9961906-A2.
XX
XX 02-DEC-1999.
XX
XX 27-MAY-1999; 99MO-US11720.
XX
XX 28-MAY-1998; 98US-0086503.
XX
XX 30-APR-1999; 99US-0303064.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX
XX Maine GT, Hunt JC, Brojanac S, Sheu MJ, Chovan LB, Tyner JD;
XX
XX Howard LV, Parmley SF, Remington JS, Araujo F, Suzuki Y, Li S;
XX
XX WPI; 2000-072663/06.
XX
XX N-PSDB; AA256330.
XX
XX Composition useful for diagnosing toxoplasmosis -
XX
XX
XX Example 11; Fig 13; 169pp; English.
XX
XX
XX The present invention describes a composition (I) comprising a
XX
XX combination of Toxoplasma gondii antigens (Ag) such as novel P29, along
XX
XX with P35 and P30/P66. (I) is useful in detecting T. gondii specific
XX
XX (immunoglobulin) IgM/IgG antibodies, which is useful in diagnosing
XX
XX toxoplasmosis. P35 antigen is useful in distinguishing between acute
XX
XX and chronic toxoplasmosis. (I) is also useful as vaccines. In combination
XX
XX with other known antigens, P29 accurately detects the presence of IgG or
XX
XX IgM in the test sample, hence eliminates the problem of false negative
XX
XX or false positive tests. T. gondii P35 IgG immunoassay detects only the
XX
XX T. gondii IgG Abs present in acute infection and does not detect IgG
XX
XX antibodies in chronic infection, which facilitates an accurate diagnosis
XX
XX of the infection stage, which is useful for the clinical management. The
XX
XX present sequence represents a fusion protein, from an example in the
XX
XX present invention.
XX
XX
XX Sequence 654 AA;
XX
XX
XX Query Match 0.6%; Score 8; DB 21; Length 654;
XX
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX QY 105 FGAGLTR 112
XX
XX |||||
XX
XX 529 FGAGLTR 536
XX
XX
XX
XX
XX RESULT 64
XX
XX ABB71989
XX
XX ID ABB71989 standard; Protein; 679 AA.
XX
XX
XX ABB71989;
XX
XX
XX 26-MAR-2002 (first entry)
XX
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 42759.
XX
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX
XX pharmaceutical.
XX
XX Drosophila melanogaster.
XX
XX
XX WO200171042-A2.
XX
XX
XX 27-SEP-2001.
XX
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX

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XX
XX (PERK ) PB CORP NY.
XX
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL16092.
XX
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX
XX interactions -
XX
XX
XX Disclosure; SEQ ID NO 42759; 21pp + Sequence listing; English.
XX
XX
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX
XX useful in developmental biology and in elucidating cell signalling and
XX
XX cell-cell interactions in higher eukaryotes for the development of
XX
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX
XX discloses genomic DNA sequences (ABL16176-ABL16511), expressed DNA
XX
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX
XX (ABBS7737-ABBS72072).
XX
XX The sequence data for this patent did not form part of the printed
XX
XX specification, but was obtained in electronic format directly from WIPO
XX
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
XX Sequence 679 AA;
XX
XX
XX Query Match 0.6%; Score 8; DB 22; Length 679;
XX
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX QY 348 MKSSAEVT 355
XX
XX |||||
XX
XX 297 MKSSAEVT 304
XX
XX
XX
XX
XX RESULT 65
XX
XX AAG79222
XX
XX ID AAG79222 standard; Protein; 845 AA.
XX
XX
XX AAG79222;
XX
XX
XX 03-JAN-2002 (first entry)
XX
XX
XX Amino acid sequence of an oxoprolinase-like enzyme polypeptide.
XX
XX
XX Human; oxoprolinase-like enzyme; OP-like enzyme; cancer; chemotherapy;
XX
XX radiation therapy.
XX
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX
XX FT Misc-difference 217
XX
XX FT Misc-difference /note= "Met encoded by TC"
XX
XX
XX WO200173056-A2.
XX
XX
XX 04-OCT-2001.
XX
XX
XX 27-MAR-2001; 2001WO-EP03427.
XX
XX
XX 27-MAR-2000; 2000US-192364P.
XX
XX
XX (FARB ) BAYER AG.
XX
XX
XX Ramakrishnan S;
XX
XX
XX WPI; 2001-616515/71.
XX
XX N-PSDB; AA165824.
XX
XX
XX New polynucleotide encoding a human oxoprolinase-like enzyme,
XX
XX regulation of which is used for enhancing chemotherapy or radiotherapy
XX
XX

```

PT of cancer cells and to protect normal cells during treatment -
 XX
 PS Example 1: Fig 4, 71pp, English.
 CC The present sequence represents a human oxoprolinase-like (OP-like)
 CC enzyme. The OP-like polynucleotide is used to produce an OP-like enzyme
 CC polypeptide, and is also used in a hybridization assay to detect
 CC similar polynucleotides. The OP-like polynucleotide or polypeptide
 CC are used to screen for compounds that decrease activity of an OP-like
 CC polypeptide, or screen for agents that regulate activity of an OP-like
 CC enzyme. An expression vector or a reagent that modulates OP-like enzyme
 CC activity is useful to treat a disease, particularly cancer. The
 CC treatment is used to enhance the effects of chemotherapy or radiation
 CC therapy of cancer cells and at the same time to protect normal cells
 CC from the toxic effects of such treatment.
 SO Sequence 845 AA;
 Query Match 0.6%; Score 8; DB 22; Length 845;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 456 PEVFGNLTN 463
 Db 618 PEVFGNLTN 625
 RESULT 66
 ABG66688 standard; Protein; 848 AA.
 XX ABG66688;
 AC 30-AUG-2002 (first entry)
 DT Human novel polypeptide #23.
 DE
 XX Human; inflammatory condition; shock; sepsis; immune response;
 KW cancer; wound healing; central nervous system disease; haematopoiesis;
 KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
 KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;
 KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
 KW bone degenerative disorder; periodontal disease; reperfusion injury;
 KW lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
 KW allergic condition; thrombolytic; thrombosis; coagulation disorder;
 KW fungal infection;
 KW Homo sapiens.
 OS
 XX WO200244340-A2.
 PN 06-JUN-2002.
 PD 30-NOV-2001; 2001WO-US47004.
 PF 30-NOV-2000; 2000US-0028952.
 PR (HYSE-) HYSEQ INC.
 PA Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D,
 PI Yamazaki V, Ujwal ML, Drmanac RT;
 DR N-PSDB; ABK94912.
 XX Novel nucleic acids and polypeptides for diagnosis, treatment of
 PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
 PT disorders, cancer and promoting wound healing -
 PS Claim 10, Page 588-589, 672pp, English.
 CC The invention relates to human novel polynucleotides and associated
 CC polypeptides. The polynucleotides and polypeptides are useful for

CC treating inflammatory conditions such as arthritis, nephritis, Crohn's
 CC disease, ischemia-reperfusion injury, shock, sepsis, immune responses
 CC and cancer and for promoting wound healing. The sequences are used to
 CC induce the proliferation of neural cells and regeneration of nerve and
 CC brain tissue, and are useful for the treatment of central and peripheral
 CC nervous system diseases and neuropathies, such as Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease and amyotrophic lateral
 CC sclerosis. The sequences are involved in chemotactic or chemokinetic
 CC activity, regulation of hematopoiesis, treatment of myeloid or lymphoid
 CC cell disorders and platelet disorders such as thrombocytopenia,
 CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
 CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
 CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
 CC disease. The sequences of the invention are also useful for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, immune deficiencies and disorders
 CC including severe combined immunodeficiency (SCID), bacterial or fungal
 CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia
 CC gravis, allergic conditions such as asthma, thrombolytic or thrombosis
 CC and coagulation disorders. Sequences ABG66666-ABG66758 represent human
 CC novel polypeptides of the invention.
 SO Sequence 848 AA;
 Query Match 0.6%; Score 8; DB 23; Length 848;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 158 EEARILAS 165
 Db 772 EEARILAS 779
 RESULT 67
 ABG66687
 ID ABG66687 standard; Protein; 906 AA.
 XX ABG66687;
 AC 30-AUG-2002 (first entry)
 DT Human novel polypeptide #22.
 DE
 XX Human; inflammatory condition; shock; sepsis; immune response;
 KW cancer; wound healing; central nervous system disease; haematopoiesis;
 KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
 KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;
 KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
 KW bone degenerative disorder; periodontal disease; reperfusion injury;
 KW lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
 KW allergic condition; thrombolytic; thrombosis; coagulation disorder;
 KW fungal infection;
 KW Homo sapiens.
 OS
 XX WO200244340-A2.
 PN 06-JUN-2002.
 PD 30-NOV-2001; 2001WO-US47004.
 PF 30-NOV-2000; 2000US-0028952.
 PR (HYSE-) HYSEQ INC.
 PA Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D,
 PI Yamazaki V, Ujwal ML, Drmanac RT;
 DR N-PSDB; ABK94911.
 XX Novel nucleic acids and polypeptides for diagnosis, treatment of
 PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell

PT disorders, cancer and promoting wound healing -

PS Claim 10; Page 586-587; 672pp; English.

CC The invention relates to human novel polynucleotides and associated
CC polypeptides. The polynucleotides and polypeptides are useful for
XX treating inflammatory conditions such as arthritis, nephritis, Crohn's
CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
CC and cancer and for promoting wound healing. The sequences are used to
CC induce the proliferation of neural cells and regeneration of nerve and
CC brain tissue, and are useful for the treatment of central and peripheral
CC nervous system diseases and neuropathies, such as Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and amyotrophic lateral
CC sclerosis. The sequences are involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
CC cell disorders and platelet disorders such as thrombocytopenia,
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
CC disease. The sequences of the invention are also useful for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, immune deficiencies and disorders
CC including severe combined immunodeficiency (SCID), bacterial or fungal
CC infections, autoimmune disorders e.g., multiple sclerosis and myasthenia
CC gravis, allergic conditions such as asthma, thrombolysis or thromboecsis
CC and coagulation disorders. Sequences ABG66666-ABG66758 represent human
CC novel polypeptides of the invention.
XX

SQ Sequence 906 AA;

Query Match 0.6%; Score 8; DB 23; Length 906;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 158 EERRARLAS 165
| | | | |
Db 830 EERRARLAS 837

RESULT 68
ABB91916
ID ABB91916 standard; Protein; 934 AA.
XX
XX ABB91916;
DT 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 1127.
XX
OS Herbicidal; plant; agriculture; herbicide.
KM Arabidopsis thaliana.
XX
XX MO200210210-A2.
PN XX
PD 07-FEB-2002.
PF 28-AUG-2001; 2001MO-EP09892.
PR 28-AUG-2001; 2001MO-EP09892.
PA (FARB) BAYER AG.
PI Tietjen K, Weidler M;
PP WPI; 2002-269010/31.
DR
XX Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
XX organisms -
XX Claim 5; SEQ ID NO 1127; 261pp + Sequence listing; English.

XX	The invention relates to identifying target proteins
CC	(AB980790-AB984016) for herbicidally active compounds, comprising
CC	aligning and comparing nucleic acid or amino acid sequences from plant
CC	with nucleic acid or amino acid sequences from non-plant organisms using
CC	suitable search parameters, where plant sequences having an E-value
CC	greater by a factor of 3 than the E-value of most similar non-plant
CC	sequences are selected. The polypeptides or nucleic acids encoding them
CC	are useful for identifying modulators. The identified modulators are
CC	useful as herbicides.
XX	
SQ	Sequence 934 AA;
OY	
Db	
	Query Match 0.6%; Score 8; DB 23; Length 934;
	Best Local Similarity 100.0%; Pred. No. 1.9e+02;
	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	939 DKSQVPTI 946 98 DKSQVPTI 105
RESULT 69	
ID	AAW21721 standard; Protein; 968 AA.
AC	AAW21721
XX	AAW21721 standard; Protein; 968 AA.
AC	AAW21721;
XX	
DT	30-SEP-1997 (first entry)
XX	
DE	SH2-A.
XX	
KM	SH2 binding domain; LexA-PcERI-gamma-CT; reporter yeast; RBL-2H3 cell;
KW	Rc-epilation-R1; detection; protein-protein interaction; phosphorylation;
KW	lysine; signal transduction pathway; activated cell-surface receptor;
KM	post-transcriptionally modified protein; mast cell activation.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Domain 8..93
FT	/label= SH2_domain
FT	Misc-difference 764
FT	/note= "encoded by NAA"
FT	Misc-difference 933
FT	/note= "encoded by NCG"
XX	
EN	US5637463-A.
PD	10-JUN-1997.
XX	
PP	04-MAY-1995; 95US-0434730.
XX	
PR	04-MAY-1995; 95US-0434730.
PA	(HOFF) HOFFMANN LA ROCHE INC.
PI	Dalton S, Kochan JP, Osborne MA;
DR	WPI: 1997-319067/29.
XX	N-PSDB; AAT77764.
XX	
PT	Detection of protein-protein interactions - dependent on
PT	post-translational modification of one of the protein, also new cDNA
XX	and protein molecules containing SH2 domains
XX	
P5	Claim 18; Fig 7; 30pp; English.
XX	
CC	The sequences given in AAW21721-22 represent proteins which contain SH2
CC	domains. These sequences were identified due to their interaction
CC	with LexA-PcERI-gamma-CT, a reporter yeast strain. The cDNA sequences
CC	were isolated from a cDNA library prepared from RBL-2H3 cells, a mast
CC	cell library which expresses Pc-epsilon-R1. These SH2 domain containing

PI Jefferson AB, Majerus PW, Pot DA, Williams LT;
 XX
 DR WPI: 1997-298053/27.
 DR N-PSDB; AAT68934.
 XX
 XX GRB2 associating polypeptide, GASPase, nucleic acids and vectors -
 PT for treating proliferative disorders such as cancer and psoriasis,
 PT and for screening agonists of inositol polyphosphate 5-phosphatase
 PT activity
 XX
 PS Claim 1; Page 52-57; 107pp; English.
 XX
 XX A novel GRB2-associating protein (AAW18327), GASPase, has inositol
 CC polyphosphate 5-phosphatase and phosphatidylinositol 5-phosphatase
 CC activities that are important in growth factor-mediated signal
 CC transduction. Its amino acid sequence was deduced from an
 CC isolated GASPase nucleic acid (AAT68934). GASPase nucleic acids,
 CC cells that express these nucleic acids, GASPase proteins and
 CC antibodies raised against them can be used in screening,
 CC therapeutic and other applications, e.g. the treatment of proliferative
 CC diseases. The polypeptides can also be used in methods for
 CC determining whether a test cpd. is an agonist or antagonist of
 CC GRB2/GASPase interaction and in methods for identifying the
 CC presence of GRB2 in a sample.
 CC
 SQ Sequence 976 AA;
 Query Match 0.6%; Score 8; DB 18; Length 976;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1075 TLPSLSL 1082
 DB 14 TLPSLSL 21
 RESULT 72
 ID AAW14002 standard; Protein; 1187 AA.
 XX
 AC AAW14002;
 XX
 DT 24-JUN-1997 (first entry)
 XX
 DE Mouse SH2-containing inositol phosphatase (SHIP).
 XX
 KW SH2-containing inositol phosphatase; SHIP.
 KW inositol polyphosphate 5-phosphatase; IP5P; src homology domain 2;
 KW SH2 domain; signal transduction; leukaemia; cancer; papilloma;
 KW atherosclerosis; HIV; autoimmune disease; bone resorption;
 KW inflammation; neurodegeneration; wound healing; diagnosis; therapy.
 XX
 OS Mus sp.
 XX
 FH Key
 FT Location/Qualifiers
 FT 5..102
 FT /label= SH2
 FT /note= "src homology domain 2"
 FT Domain
 FT 549..664
 FT /label= 5-Phosphatase_domain
 FT Region
 FT 583..590
 FT /label= 5-Phosphatase_motif
 FT 659..676
 FT /label= 5-Phosphatase_motif
 FT Region
 FT 910..914
 FT /label= PTB
 FT /note= "phosphotyrosine binding domain target"
 FT Region
 FT 1013..1018
 FT /label= PTB
 FT /note= "phosphotyrosine binding domain target"
 FT 959..1145
 FT /label= Prolin-rich_domain
 FT
 XX

PN W09712039-A2.
 XX
 PD 03-APR-1997.
 XX
 XX
 PF 27-SEP-1996; 96WO-CA00655.
 XX
 PR 14-JUN-1996; 96US-0664962.
 PR 27-SEP-1995; 95US-0006063.
 PR 30-NOV-1995; 95US-0007788.
 PR 09-APR-1996; 96US-0015217.
 XX
 PA (KXYS/) KRYSTAL G.
 XX
 XX
 PI Kystal G;
 XX
 DR WPI: 1997-212898/19.
 DR N-PSDB; AAT60300.
 XX
 XX Inositol polyphosphate-5-phosphatase having SH2 domain - useful for
 PT treating cancer and other conditions involving abnormal signalling
 PT
 PS Claim 3; Page 34-38; 89pp; English.
 XX
 CC Murine inositol polyphosphate 5-phosphatase having an SH2 domain
 CC (SHIP) (AAW14002) is involved in the control of gene expression and
 CC differentiation, proliferation, activation and metabolism of cells,
 CC partic. via the Ras and phospholipid signalling pathways. It
 CC associates with Shc (see also AAW14005) in response to multiple
 CC cytokines. Recombinant SHIP can be produced in transformed host
 CC cells utilising a nucleic acid (AAT60300) obtd. from B6Sutai cells.
 CC SHIP can be used to identify substances which affect the binding of
 CC the protein to Shc and/or its inositol phosphatase activity and
 CC to screen for (ant)agonists useful for treating cancer and other
 CC conditions involving abnormal signalling. Human SHIP (AAW14003) has
 CC also been identified.
 CC
 SQ Sequence 1187 AA;
 Query Match 0.6%; Score 8; DB 18; Length 1187;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1075 TLPSLSL 1082
 DB 226 TLPSLSL 233
 RESULT 73
 ID AAW14003 standard; Protein; 1187 AA.
 XX
 AC AAW14003;
 XX
 DT 24-JUN-1997 (first entry)
 XX
 DE Human SH2-containing inositol phosphatase (SHIP).
 XX
 KW SH2-containing inositol phosphatase; SHIP;
 KW inositol polyphosphate 5-phosphatase; IP5P; src homology domain 2;
 KW SH2 domain; signal transduction; leukaemia; cancer; papilloma;
 KW atherosclerosis; HIV; autoimmune disease; bone resorption;
 KW inflammation; neurodegeneration; wound healing; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Location/Qualifiers
 FT 5..102
 FT /label= SH2
 FT /note= "src homology domain 2"
 FT Domain
 FT 549..630
 FT /label= 5-Phosphatase_domain
 FT 583..589
 FT /label= 5-Phosphatase_motif
 FT
 XX

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FT Region 658..677
FT /label= 5-Phosphatase_motif
FT Region 909..913
FT /label= PTB
FT /note= "phosphotyrosine binding domain target"
FT Region 1016..1020
FT /label= PTB
FT /note= "phosphotyrosine binding domain target"
FT Domain 961..1142
FT /label= Proline-rich_domain
FT
FT WO9712039-A2.
FT
FT 03-APR-1997.
FT
FT 27-SEP-1996; 96WO-CA00655.
FT
FT 14-JUN-1996; 96US-0664962.
FT 27-SEP-1995; 95US-0006063.
FT 30-NOV-1995; 95US-0007788.
FT 09-APR-1996; 96US-0015217.
FT
FT (KRYSTAL) KRYSTAL G.
FT
FT KRYSTAL G.
FT
FT WPI: 1997-212898/19.
FT N-PSDB; AAT60301.
FT
FT Inositol polyphosphate-5-phosphatase having SH2 domain - useful for
FT treating cancer and other conditions involving abnormal signalling
FT
FT Claim 6; Page 49-54; 89pp; English.
FT
FT
FT Human inositol polyphosphate 5-phosphatase having an SH2 domain
FT (SHIP) (AAW14003) is involved in the control of gene expression and
FT differentiation, proliferation, activation and metabolism of cells,
FT partic. via the Ras and phospholipid signalling pathways. It
FT associates with Shc (see also AAW14005) in response to multiple
FT cytokines. Recombinant SHIP can be produced in transformed host
FT cells utilizing a nucleic acid (AAT60301) obtd. from a MO7e/MO7-ER
FT cDNA library. SHIP can be used to identify substances which affect
FT the binding of the protein to Shc and/or its inositol phosphatase
FT activity and to screen for (ant)agonists useful for treating cancer
FT and other conditions involving abnormal signalling.
FT
FT Sequence 1187 AA;
FT
FT
FT Query Match 0.64; Score 8; DB 18; Length 1187;
FT Best Local Similarity 100.04; Pred. No. 2.4e+02;
FT Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT
FT 1075 TLPSLESL 1082
FT |||||
FT 225 TLPSLESL 232
FT
FT RESULT 74
FT AAW26623
FT ID AAW26623 standard; Protein: 1189 AA.
FT
FT AC AAW26623;
FT
FT 28-JAN-1998 (first entry)
FT
FT Signalling inositol polyphosphate 5-phosphatase SIP-130.
FT
FT SIP-130; signalling inositol polyphosphate 5-phosphatase; human;
FT signal transduction; phosphatidylinositol 3'-kinase;
FT mitogen activated protein kinase; MAP kinase;
FT phosphatidylinositol (3',4',5) triphosphatase; calcium signalling;
FT mitogen; cell growth; cell proliferation; apoptosis; gene delivery;
FT gene therapy.
FT

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XX OS Homo sapiens.
XX FH Key
XX Domain
XX Peptide
XX Location/Qualifiers
XX 5..103
XX /label= SH2
XX 583..591
XX /note= "conserved motif of inositol polyphosphate
XX 5-phosphatase family"
XX 669..676
XX /note= "conserved motif of inositol polyphosphate
XX 5-phosphatase family"
XX 912..915
XX /label= SHC-PTB
XX 110..1022
XX /label= SHC-PTB
XX 1106..1109
XX /label= SH3
XX /note= "SH3"
XX 1121..1124
XX /note= "proline-rich SH3 binding motif"
XX /label= SH3
XX /note= "proline-rich SH3 binding motif"
XX 1134..1137
XX /label= SH3
XX /note= "proline-rich SH3 binding motif"
XX 1139..1144
XX /label= SH3
XX /note= "proline-rich SH3 binding motif"
XX 1179..1182
XX /label= SH3
XX /note= "proline-rich SH3 binding motif"
XX 186..200
XX /note= "proline-rich SH3 binding motif"
XX 265..278
XX /note= "isolated peptide"
XX 357..365
XX /note= "isolated peptide"
XX 434..443
XX /note= "isolated peptide"
XX 570..579
XX /note= "isolated peptide"
XX 789..807
XX /note= "isolated peptide"
XX 701..721
XX /note= "isolated peptide"
XX 746..760
XX /note= "isolated peptide"
XX
XX WO9722690-A2.
XX
XX 26-JUN-1997.
XX
XX 06-DEC-1996; 96WO-US19515.
XX
XX 04-DEC-1996; 96US-0759397.
XX 08-DEC-1995; 95US-0569578.
XX 14-DEC-1995; 95US-0008607.
XX 28-MAR-1996; 96US-0624190.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Kavanagh WM, Pot D, Williams LT;
XX WPI: 1997-341681/31.
XX N-PSDB; AAT90500.
XX
XX Signalling inositol polyphosphate 5-phosphatase, SIP 130 and
XX related DNA - used for treating abnormal cell growth, regulating
XX mitogenic activity and calcium signalling
XX Claim 1; Page 87-91; 114pp; English.
XX
XX This polypeptide comprises a novel signalling inositol polyphosphate
XX

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